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(54) Title: SYSTEM FOR GENETICALLY TREATING CARDIAC CONDUCTION DISTURBANCES		
(57) Abstract		
<p>The present invention provides delivery systems for delivering conduction protein genetic material to cardiac cells in localized areas of the heart to improve the conductance therein. More specifically, there is provided a system for delivering connexin proteins or nucleic acid molecules encoding connexin proteins to a site in the heart which has been determined by mapping procedures to have a conduction disturbance. For cases where conduction is impaired, selected genetic material is delivered by Applicants' delivery system to cells around the disturbance area, in order to enhance overall conductivity patterns; in other cases, genetic material is selected to slow conduction in affected areas, so as to prevent, e.g., brady-tachy syndrome.</p>		

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**SYSTEM FOR GENETICALLY TREATING  
CARDIAC CONDUCTION DISTURBANCES**

**FIELD OF THE INVENTION**

The present invention relates to systems for  
5 delivering conduction protein genetic material to cardiac  
cells in localized areas of the heart to improve the  
conductance therein.

**BACKGROUND OF THE INVENTION**

The conduction system of the human heart is  
10 normally automatic, resulting in the contraction of the  
atria and ventricles by means of electrical impulses that  
originate in cardiac tissue. The cardiac cycle is separated  
into the contraction phase (systole) and relaxation phase  
(diastole). Although the rhythm of the cardiac cycle is  
15 intrinsic, the rate of this rhythm is modified by autonomic  
nerves and hormones such as epinephrine. The autonomic  
nervous system is comprised of parasympathetic and  
sympathetic nerves which release neurotransmitters such as  
acetylcholine and norepinephrine, respectively.

20 The natural pacemaker of the human heart is  
located in the posterior wall of the right atrium in a small  
area, approximately 2 by 5 by 15 mm, referred to as the  
sinoatrial node (SA node). The SA node initiates the  
cardiac cycle of systole and diastole phases by generating  
25 an electrical impulse that spreads over the right and left  
atria, causing them to contract almost simultaneously. This  
electrical impulse, referred to as the pacemaker potential,

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is created by the depolarization of the myocardial cells of the SA node, which results from changes in membrane permeability to cations. When the cell membrane is depolarized to about -30 mV, an action potential is  
5 produced. This impulse then passes to the atrioventricular node (AV node), which is located on the inferior portion of the interatrial septum. The impulse then continues through the atrioventricular bundle, referred to as the bundle of His, which is located at the top of the interventricular  
10 septum. The bundle of His divides into right and left branches which lead to the right and left ventricles respectively. Continuous with both branches of the bundle of His are the Purkinje fibers, which terminate within the ventricular walls. Stimulation of these fibers causes the  
15 ventricles to contract almost simultaneously and discharge blood into the pulmonary and systemic circulatory systems.

Abnormal patterns of electrical conduction in the heart can produce abnormalities of the cardiac cycle and seriously compromise the function of the heart, sometimes  
20 being fatal. For example, patients having such cardiac conduction disturbances may suffer from sick sinus syndrome (SSS), "brady-tachy syndrome," bradycardia, tachycardia, and heart block. Artificial pacemakers are often used in patients which suffer from these cardiac conduction  
25 disturbances.

In SSS, the conduction problem relates to, *inter alia*, intermittent reentry of the electrical impulse within the nodal tissue, sometimes resulting in rapid heart beats. A dual chamber pacemaker is often used to sense atrial  
30 activity and control the ventricle at the appropriate rate.

In some congenital diseases such as "brady-tachy syndrome," bradycardia, a slow rate of impulse, and tachycardia, a rapid rate of impulse, occur intermittently. The disease can be fatal where long pauses allow premature  
35 ventricular contractions (PVCs) to occur in multiples, initiating tachycardia. A pacemaker and/or cardioverter can be used to control episodes of tachycardia, and conventional

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demand type pacemakers have long been effective in treating bradycardia.

Excessive delay or failure of impulse transmission in abnormally slow impulse conduction is known as heart  
5 block. Heart block is often caused by scar tissue disrupting the conduction system. The cardiac impulse is believed to normally spread from the SA node along internodal pathways to the AV node and ventricles within 0.20 seconds. Heart block occurs in three progressively  
10 more serious stages. In first-degree heart block, although all impulses are conducted through the AV junction, conduction time to the ventricles is abnormally prolonged. In second-degree heart block, some impulses are conducted to the ventricles, whereas some are not. In third-degree heart  
15 block, no impulses from the natural pacemaker are conducted to the ventricles. This results in a slower ventricular contraction rate. The rate of contraction in this case is usually determined by the rate of the fastest depolarizing His-Purkinje cell distal from the block site. Typically,  
20 heart rates in third-degree block are in the 20 to 60 bpm range, but can also be as low as zero in some cases.

Arrhythmias resulting from cardiac conduction disturbances can be treated with a variety of drugs that inhibit specific aspects of the cardiac action potentials  
25 and inhibit the production or conduction of impulses along abnormal pathways. Drugs used to treat these arrhythmias block the fast Na<sup>+</sup> channels (quinidine, procainamide, lidocaine), block the slow Ca<sup>++</sup> channel (verapamil), or block β-adrenergic receptors (propranolol).

30 The cardiac conduction system, or electrical activation of the heart, involves the transfer of current, in the form of chemical ion gradients, from one myocardial cell to another. Conductive proteins in cardiac cells facilitate this transfer of current. Individual cardiac  
35 cells express a plurality of gap junction channel proteins, through which ions traverse. The intercellular channels of gap junctions are assembled from individual membrane-

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spanning connexin proteins, several of which have been cloned and sequenced in mammals. These proteins facilitate the transfer of ions from cell to cell and are responsible for electronic coupling of cells. Saffitz, et al., *J. Card.*

5 *Electophys.*, 1995, 6, 498-510.

Connexin proteins comprise a family of related proteins and include, for example, Cx43 (Fishman, et al., *J. Cell Biol.*, 1990, 111, 589-598), and Cx40 and Cx45 (Kanter, et al., *J. Mol. Cell Cardiol.*, 1994, 26, 861-868). Cx43 10 appears to be the most abundant connexin in the heart, with expression in the ventricle and atrial myocardium, and distal bundle of His and Purkinje fibers, while being absent from the SA node, AV node, and proximal bundle of His. Gourdie, et al., *J. Cell Sci.*, 1993, 105, 985-991, and 15 Davis, et al., *J. Am. Coll. Cardiol.*, 1994, 24, 1124-1132. Cx40 is most abundantly expressed in the atrial myocardium, and in the distal bundle of His and Purkinje fibers, while present at reduced levels in the ventricular myocardium, and the nodes. Gourdie, et al., *J. Cell Sci.*, 1993, 105, 985- 20 991, and Davis, et al., *J. Am. Coll. Cardiol.*, 1994, 24, 1124-1132. Cx45 is moderately expressed in the ventricle and atrial myocardium, and distal bundle of His and Purkinje fibers, while present at lower levels in the SA node, AV node, and proximal bundle of His. Gourdie, et al., *J. Cell 25 Sci.*, 1993, 105, 985-991, and Davis, et al., *J. Am. Coll. Cardiol.*, 1994, 24, 1124-1132. Cx43 and Cx40 connexins are relatively fast conductive proteins, whereas Cx45 is a relatively slow conductive protein.

Gene therapy has recently emerged as a powerful 30 approach to treating a variety of mammalian diseases. Direct transfer of genetic material into myocardial tissue *in vivo* has recently been demonstrated to be an effective method of expressing a desired protein. For example, direct myocardial transfection of plasmid DNA by direct injection 35 into the heart of rabbits and pigs (Gal, et al., *Lab. Invest.*, 1993, 68, 18-25), as well as of rats (Ascadi, et al., *The New Biol.*, 1991, 3, 71-81), has been shown to

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result in expression of particular reporter gene products. In addition, direct *in vivo* gene transfer into myocardial cells has also been accomplished by directly injecting adenoviral vectors into the myocardium. French, et al., 5 *Circulation*, 1994, 90, 2415-2424, and PCT Publication WO 94/11506.

It has long been desired to effectively treat conduction pathway abnormalities. To this end, conventional procedures including drug therapy, pacemaker technology, or 10 a combination thereof, have been employed. In contrast to these therapeutic procedures, Applicants' invention is directed to delivery systems for treating and/or correcting disturbances in the cardiac conduction pathway by delivering conduction protein genetic material into myocardial tissue. 15 In patients with cardiac conduction disturbances, it is desirable to locate the problematic area within the heart, and either treat the problematic cells to restore proper cardiac conduction or enhance the cardiac conduction of normal cells surrounding the problematic area. For example, 20 in a patient with heart block, a tract of normal, healthy cells surrounding the scar in the ventricle, which is causing the heart block, is identified and treated with Applicants' delivery system by expressing cardiac conduction proteins, such as, for example, gap junction proteins to 25 impart a faster or otherwise enhanced conduction system. In this case, the block can be effectively bridged, or shunted, resulting in a QRS of a width intermediate between a normally conducted beat and a PVC.

#### SUMMARY OF THE INVENTION

30 In accordance with the above, the primary purpose of Applicants' claimed invention is to provide delivery systems for treating cardiac conduction disturbances. Upon identifying a problematic area within the heart, conduction protein genetic material is selected such that expression of 35 a selected conduction protein corrects or improves the cardiac conduction of the cells in the problematic area.

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Alternatively, expression of a selected conduction protein can improve the cardiac conduction of normal, healthy cells surrounding the problematic cells. Improvement of cardiac conduction can be manifested by a replacement, a speeding up, or a slowing down of the existing conduction pathway.

The conduction protein genetic material comprises recombinant nucleic acid molecules comprising a nucleic acid molecule encoding the conduction protein inserted into a delivery vehicle, such as, for example, plasmids or adenoviral vectors, and the appropriate regulatory elements.

Alternatively, the conduction protein genetic material comprises the conduction protein itself. Expression of the desired conduction protein from recombinant nucleic acid molecules is controlled by promoters, preferably cardiac tissue-specific promoter-enhancers, operably linked to the nucleic acid molecule encoding the conduction protein. The conduction protein is preferably a gap junction protein, such as, for example, the connexins Cx40, Cx43, and Cx45, which is used to correct or improve the cardiac conduction of cells within the problematic area. For example, if the cardiac conduction pathway disturbance is a heart block or bradycardia, Cx43 or Cx40 is preferably used. However, if the cardiac conduction pathway disturbance is tachycardia, Cx45 is preferably used. The cardiac conduction genetic material is delivered to specific sites within the heart by perfusion or injection of a therapeutically effective amount, which is that amount which corrects or improves the cardiac conduction of the myocardial cells. The therapeutically effective amount can be delivered to the specific site in the heart in a single dose or multiple doses, as desired.

The present invention provides a delivery system for delivering a therapeutically effective amount of a predetermined conduction protein genetic material to an identified cardiac location, the genetic material being selected for altering the conductivity of cardiac cells to which it is delivered. The delivery system includes the

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selected genetic material contained in a reservoir, and a catheter subsystem for delivering the genetic material from the reservoir to the identified cardiac location so as to contact a plurality of cells in the proximity of the  
5 selected cardiac location.

The delivery system may utilize an external reservoir for providing the genetic material, or alternately may utilize an implantable reservoir. In either embodiment, a controllable pump mechanism is provided for transferring  
10 therapeutic doses of the genetic material from the reservoir, through a catheter, and to the selected cardiac location. The catheter subsystem may be of a type for direct introduction into the myocardium, as with a transthoracic procedure, or, more preferably, a endocardial  
15 catheter having a distal tip portion adapted for positioning and injecting the genetic material into the myocardium from within a heart chamber. In a preferred embodiment, the catheter distal tip has a normally withdrawn helical needle, which is extendable when positioned in the vicinity of the  
20 selected site so as to be screwed into the heart. The needle is hollow and connects with the catheter lumen so as to receive the pumped genetic material; it has one or more ports located so as to effectively release the genetic material for transduction into the mapped area. In another  
25 preferred embodiment of the invention, the delivery system is combined with the mapping catheter such that once the selected site is identified, the delivery system, which is within the mapping catheter, is engaged without removing the mapping catheter. The delivery system can be used for one  
30 treatment and then removed, or can be implanted for subsequent treatments, in which latter case it is controllable by an external programmer type device.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a flow diagram presenting the primary  
35 steps involved in the practice of this invention, including mapping the patient's conductive system to determine the

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location of the problem, choosing an appropriate genetic material, and expressing the genetic material in an appropriate dose into the determined location.

Figure 2 is a schematic representation of a delivery system in accordance with this invention, illustrating delivery of genetic material into a patient's heart at the chosen location.

Figure 3 is a schematic drawing of the distal portion of a catheter, which can be extendable and retractable, used for injecting a solution carrying chosen genetic material into a patient's heart.

Figure 4 illustrates the distal end of a catheter, having a distal portion which encloses an osmotic pump.

Figure 5 illustrates a delivery system in which the delivery means comprises a mapping catheter combined with a delivery system for injecting a solution carrying chosen genetic material into a patient's heart.

Figure 6A is a schematic representation of a delivery system in accordance with this invention, having a combined catheter and pacing lead, with a separate pump; Figure 6B is another embodiment of a combined pacing lead and delivery catheter having a reservoir located at the distal end of the catheter.

#### DESCRIPTION OF THE PREFERRED EMBODIMENTS

Applicants' invention provides delivery systems for treating cardiac conduction pathway disturbances. A problematic area exhibiting, for example, SSS, "brady-tachy syndrome," bradycardia, tachycardia, or heart block, within the heart is identified by routine and conventional techniques known to the skilled artisan. Once the specific problem has been identified, conduction protein genetic material is selected such that expression of a selected conduction protein corrects or improves the cardiac conduction of the problematic cells or improves the cardiac conduction of normal cells surrounding the problematic cells. The conduction protein genetic material comprises

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either the conduction protein itself or recombinant nucleic acid molecules comprising a nucleic acid molecule encoding the conduction protein inserted into a delivery vehicle, such as, for example, plasmid, cosmid, YAC vector, viral vectors, and the like, and the appropriate regulatory elements. In preferred embodiments of the present invention, the nucleic acid molecule encoding the conduction protein is the full length coding sequence cDNA of a conduction protein, and is inserted into a plasmid or 5 adenoviral vector, such as, for example, pGEM3 or pBR322, and Ad5, respectively. The regulatory elements are capable of directing expression in mammalian cells, specifically human cells. The regulatory elements include a promoter and a polyadenylation signal. Expression of the desired 10 conduction protein is preferably controlled by cardiac tissue-specific promoter-enhancers, operably linked to the nucleic acid molecule encoding the conduction protein. The conduction protein is preferably a gap junction protein, such as, for example, the connexins Cx40, Cx43, and Cx45, 15 which is used to correct or improve the cardiac conduction of cells within the problematic area. The specific gap junction protein chosen is dependent upon the nature of the identified problem. For example, where the conduction is slow or non-existent, such as in heart block or bradycardia, 20 introduction of Cx40 or Cx43 would enhance conduction. In contrast, introduction of the slower conducting Cx45 into the AV node and His tissues would result in the prevention of brady-tachy syndrome and tachycardia. The conduction protein genetic material is preferably delivered in a 25 pharmaceutical composition comprising, for example, the conduction protein genetic material in a volume of phosphate-buffered saline with 5% sucrose. The cardiac conduction genetic material is delivered to specific sites 30 within the heart by perfusion or injection of a therapeutically effective amount, which is that amount which 35 corrects or improves the cardiac conduction of the myocardial cells. The therapeutically effective amount can

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be delivered to the specific site in the heart in single or multiple doses, as desired, using the delivery systems of the invention.

The present invention comprises a delivery system  
5 for delivering a therapeutically effective amount of conduction protein genetic material to a mapped cardiac location in such a way as to enhance the effective conduction of the myocardial cells around the area of disturbance. In a first embodiment, the delivery system  
10 basically comprises a reservoir subsystem for holding the genetic material, and a catheter subsystem in communication with the reservoir subsystem for placement of the genetic material in and around the identified cardiac location. As seen in the following discussion of several preferred  
15 embodiments, the reservoir subsystem and catheter subsystem may be separate, or they may be combined. Preferably the reservoir contains up to 25 ml of a genetic material for delivery to the myocardium. In some applications, only a bolus of about 0.1-10 ml, or more preferably 1-5 ml, is  
20 delivered to the targeted areas. In other applications, such as where conduction protein is being delivered in repeated doses, 25 ml or more may be used. Also, the genetic material may be diluted in a saline solution, such as, for example, phosphate-buffered saline (PBS), the  
25 reservoir holding the diluted solution for controlled delivery. Additionally, it is to be understood that the reservoir and associated control apparatus may be either implantable or external to the body, depending upon the circumstances, e.g., whether metered doses are to be  
30 administered to the patient over a period of time, or whether the delivery of the genetic material is essentially a one time treatment.

Referring now to Fig. 1, the primary steps involved in the practice of this invention are shown in the  
35 flow diagram. As illustrated in 30, the first step is to determine the nature of the cardiac conduction disturbance, which can manifest itself in ineffective or harmful

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conductive properties. This step can constitute diagnosis of SSS, "brady-tachy syndrome," bradycardia, tachycardia, heart block, etc. The next step, illustrated in 32, is mapping the patient's heart to determine the location, size 5 and extent of the disturbance of problematic area. Intracardiac electrocardiographic techniques, or electrophysiology (EP) studies, permit a detailed analysis of the mechanisms of cardiac impulse formation and conduction. The testing and mapping protocol utilized and 10 the sites selected for recording depend upon the symptoms manifested in the individual. One skilled in the art is readily familiar with cardiac mapping techniques, such as, for example, those described in U.S. Patent 4,699,147, U.S. Patent 5,297,549, and U.S. Patent 5,397,339, all of which 15 are incorporated by reference. The mapping techniques known to those skilled in the art will readily identify those cardiac locations encompassing cardiac cells with abnormal conduction properties. As shown in 33, the next step is to select the appropriate conduction protein genetic material. 20 This selection, which yields the "preselected genetic material," is dependent upon the nature of the cardiac conduction disturbance, as discussed below. The conduction protein genetic material is next prepared, as illustrated in 34, by either inserting the nucleic acid molecules encoding 25 the appropriate conduction protein into a delivery vehicle with the appropriate regulatory elements, in the case of a recombinant nucleic acid molecule, or expressing the conduction protein from an expression vector, in the case of the conduction protein itself. As shown in 35, the next 30 step is to prepare and load the delivery system with a therapeutically effective amount of the conduction protein genetic material. As illustrated in 37, the next step comprises administering the therapeutically effective amount to the patient by contacting the appropriate location in the 35 heart, as determined earlier, using the delivery system described herein. An alternative method of administering the therapeutically effective amount of the conduction

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protein genetic material is to directly inject the heart of the patient. The final step, shown in 38, is to evaluate the response of the patient to the treatment.

Referring now to Fig. 2, there is shown an 5 illustrative embodiment of a delivery system useful for certain applications of this invention, e.g., where larger amounts of genetic material alone or in solution are employed. A catheter 36, preferably a transvenous catheter, includes an elongated catheter body 40, suitably an 10 insulative outer sheath which may be made of polyurethane, Teflon, silicone, or any other acceptable biocompatible plastic. The catheter has a standard lumen (illustrated in Fig. 3) extending therethrough for the length thereof, which communicates through to a hollow helical needle element 44, 15 which is adapted for screwing into the patient's myocardium. The outer distal end of helical element 44 is open, permitting genetic material in fluid form to be dispensed out of the end, as is discussed in more detail below in connection with Fig. 3. At the proximal end of the 20 catheter, a fitting 46 is located, to which a Luer lock 48 is coupled. Luer lock 48 is coupled to the proximal end of elongated catheter body 40 and receives the lumen. A swivel mount 50 is mounted to Luer lock 48, allowing rotation of the catheter relative to Luer lock 52. Luer lock 52 in turn 25 is coupled through control element 54 to a tube 58 which communicates with reservoir 55, suitably through flow control 57 and filter 56. Reservoir 55 holds a supply of the selected genetic material. Control elements 57 and 54 are used for adjustment of the pressure and flow rate, and 30 may be mechanically or electronically controlled. Thus, unit 54 or 57 may be used to control either rate of delivery, or dosage size, or both. Control unit 54 may be programmed to automatically release predetermined doses on a timed basis. Further, for an implanted system, control unit 35 54 may be activated from an external programmer as illustrated at 51. Reference is made to international application published under the PCT, International

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Publication No. WO 95/05781, incorporated herein by reference, for a more detailed description of such a reservoir and catheter combination. It is to be understood that such a system is useful for this invention only for 5 applications where larger fluid amounts are to be expressed, e.g., where a diluted saline solution is used to wash or perfuse a selected area.

Referring now to Fig. 3, there is shown in expanded detail a schematic of the distal end of the 10 catheter of Fig. 2, illustrating the interconnection of the helical element 44 with the interior of the catheter. As illustrated, the helical needle 44 is provided with an internal lumen 59 which is in communication with the internal lumen 63L of the lead formed by tube 63. In this 15 embodiment, helical element 44 may also be a pacing electrode, in which case it is formed of conductive material and welded, crimped, swaged, or connected by other means so as not to prevent fluid flow, to tip element 61. Tip element 61 in turn is electrically connected to a conductor 20 coil or coils 64, 65, which extend the length of the lead and are connected to a pacemaker. An outer membrane 60 forms the outer wall of elongated catheter body 40, shown in Fig. 2. Further referring to Fig. 3, element 44 has an outlet 75 where the genetic material may be expressed, and 25 holes or ports 76, 77, and 78 may also be utilized for providing exits for the genetic material which is supplied through lumen 59 under a pressure of up to about one atmosphere from reservoir 55 and the control elements.

In practice, a catheter 36 of the form illustrated 30 in Figs. 2 and 3 is advanced to the desired site for treatment, which site or location has been previously identified by means of cardiac mapping, as discussed above. The catheter may be guided to the indicated location by being passed down a steerable or guidable catheter having an 35 accommodating lumen, for example as disclosed in U.S. Patent No. 5,030,204; or by means of a fixed configuration guide catheter such as illustrated in U.S. Patent No. 5,104,393.

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Alternately, the catheter may be advanced to the desired location within the heart by means of a deflectable stylet, as disclosed in PCT Patent Application WO 93/04724, published March 18, 1993, or by a deflectable guide wire as 5 disclosed in U.S. Patent No. 5,060,660. In yet another embodiment, the helical element 44 may be ordinarily retracted within a sheath at the time of guiding the catheter into the patient's heart, and extended for screwing into the heart by use of a stylet. Such extensible helical 10 arrangements are commercially available and well known in the pacing art.

It is to be understood that other forms of the reservoir subsystems and catheter subsystems are within the scope of this invention. Reservoir embodiments include, for 15 example, drug dispensing irrigatable electrodes, such as those described in U.S. Patent 4,360,031; electrically controllable, non-occluding, body implanting drug delivery system, such as those described in U.S. Patent No. 5,041,107; implantable drug infusion reservoir such as those 20 described in U.S. Patent No. 5,176,641; medication delivery devices such as those described in U.S. Patent 5,443,450; and infusion pumps, such as SYNCHROMED® made by Medtronic, Inc.; and osmotic pumps such as those made by Alza.

Referring now to Fig. 4, there is shown, by way of 25 illustration, another embodiment of a delivery system having a combined catheter and reservoir, useful for applications involving delivery of a relatively small bolus of genetic material, e.g., 1-5 ml. Fig. 4 illustrates the distal end of a catheter, having a distal portion 70 which encloses an 30 osmotic pump. See U.S. Patent 4,711,251, assigned to Medtronic, Inc., incorporated herein by reference. The pump includes an inner chamber 68 and an outer chamber 66, which chambers are separated by an impermeable membrane 67. A semi-permeable outer membrane 72 forms the outer wall of 35 chamber 66. The tubular portion 74 of the helical member connects to lumen 74L within inner chamber 68. A conductor 80, which runs the length of the catheter, extends into the

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inner chamber 68 and connects with extension 74E as shown at 74C to provide electrical contact through to element 44, in an application which the element 44 is used as a pacing electrode. A seal 79 is provided at the point where the 5 conductor passes through outer membrane 72 and inner membrane 67. An insulating cover 86 encompasses the conductor 80 from the point of contact with seal 79. An end cap 73, which may be integral with outer membrane 72 closes the chamber. Alternately, end cap 73 may be constructed to 10 elute a predetermined medication, such as, for example, steroids. Steroids, such as dexamethasone sodium phosphate, beclamethasone, and the like, are used to control inflammatory processes.

In this arrangement, prior to inserting the 15 catheter distal end into the patient's heart, the inner chamber 68 is charged with the genetic material which is to be dispensed into the myocardium. This may be done, for example, by simply inserting a micro needle through end cap 73, and inserting the desired bolus of genetic material into 20 chamber 68. After the chamber 68 is filled and the catheter is implanted, body fluids will enter chamber 66 through membrane 72 to impart a pressure on the inner chamber 68 via the impermeable membrane 67. This results in a dispensing of the genetic material stored within chamber 25 68 through the lumen 74L of extension 74E and the helical element 44. Although the preferred needle or element 44 is helical, additional configurations of needles or elements can also be used as known to those skilled in the art.

Still referring now to Fig. 4, there is 30 illustrated another embodiment of a catheter tip useful for delivering a small bolus of the selected genetic material. In this embodiment, the bolus of material is stored within the hollow interior of helical element 44, i.e., the interior is the reservoir. The interior reservoir is 35 maintained sealed by use of a soluble material which is normally solid, but which dissolves when subjected to body fluids for a period of time. An example of such material is

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mannitol, which can be used when the delivery system is not preloaded with the conduction protein genetic material. Plugs or globules 81-85 of mannitol are illustrated (by dashed lines) in place to block the two ends of element 44, 5 as well as the ports 76, 77, 78. In instances where the conduction protein genetic material is preloaded into the delivery system, a shape memory metal can be used in place of the mannitol. Such metals are well known to the skilled artisan. Either of these features can be combined with an 10 osmotic pump, as described in connection with Fig. 3, where the outer chamber is filled with a saline solution which forces the genetic material out of the ports of element 44. Alternatively, the outer chamber can be filled with the 15 genetic material, which is then forced out of the ports of element 44. Another alternate embodiment, not shown, is to use a stylet which inserted through to the distal end of the catheter, to push a piston which aids in expressing the genetic material into the myocardial cells.

Although a transvenous form of delivery system is 20 preferred, it is to be understood that the invention can employ other methods and devices. For example, a small bolus of selected genetic material can be loaded into a micro-syringe, e.g., a 100  $\mu$ l Hamilton syringe, and applied directly from the outside of the heart.

25 Referring now to Fig. 5, there is shown, by way of illustration, another embodiment of a delivery system having a combined mapping catheter and delivery means. The delivery system of this embodiment comprises a catheter 90 with a distal end 91 having an opening at the distal end. 30 The catheter 90 further comprises mapping electrode means 92 at the distal end 91. The mapping electrode means carries out the mapping of the patient's heart. Conductor means 93 electrically connects the mapping electrode means 92 to the proximal end 94 of the catheter 90. The delivery system 35 further comprises a delivery means within the catheter. The embodiment of the delivery means illustrated in Fig. 5 is the delivery means shown in Fig. 3. However, any of the

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delivery means described herein can be used in combination with the mapping catheter shown in Fig. 5. The catheter 90 is inserted into the patient's heart and the site located by routine mapping procedures. Once a site is identified in 5 the heart, the mapping catheter 90 remains in place and the delivery means is then extended through the distal end 91 of the catheter 90, and the heart tissue or cells is contacted with the conduction protein genetic material. In another embodiment of the invention, the catheter 90 is a peelable 10 introducer sheath, with two conductor means 93 electrically connecting the introducer sheath, which serves to map the heart, to electrode means 92. Once the cardiac site is mapped, the delivery means is contacted with the heart tissue, and the introducer is removed and peeled away.

15 Referring now to Fig. 6A, there is shown, by way of illustration, another embodiment of an implantable delivery system comprising a combined pacing lead and delivery catheter, hereinafter referred to simply as a catheter. In this embodiment, the catheter 90 is combined 20 with a pacemaker or pulse generator (not shown) and a source of genetic material such as illustrated by pump 100 which is suitably implanted near the pacemaker. The proximal end 101 of the catheter is connected to the pacemaker in the standard fashion. The genetic material is delivered through 25 connecting tube 102 to a proximal section 88 of the catheter, communicating with lengthwise catheter lumen illustrated at 89. Alternately, the pacemaker head may contain a reservoir and micropump, for providing delivery of the genetic material directly to the lumen 89. The main 30 length of the catheter has an outside sheath of biocompatible insulating material 96, and at least one conductor coil 95 which communicates electrically from the pacemaker to electrode 97 at the distal tip of the catheter. The catheter further comprises an axially positioned 35 polymeric cannula 103, having lumen 87, through at least a portion of the catheter length and positioned within coil 95, which provides an inner surface for the catheter lumen.

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The cannula terminates at the distal end of the catheter, just proximal to the tip portion of electrode 97, which is illustrated as having an outer porous surface. Electrode 97 has a central opening, shown covered with the porous 5 electrode material, through which genetic material can pass when the catheter is positioned in the patient. As shown, conductor coil 95 is electrically connected to electrode 97, and connects pace pulses and sensed cardiac signals between the pacemaker and the electrode. Of course, for a bipolar 10 embodiment, the lead/catheter 90 carries a second electrode (not shown), suitably a ring electrode just proximal to electrode 97. Also, as illustrated, a fixation mechanism such as tines 98 are employed for fixing or anchoring the distal tip to the heart wall of the patient.

15 In one embodiment, pump 100 is suitably an osmotic minipump, which pumps fluid contained within through tube 102, into catheter portion 88 and through lumens 89, 87 to the tip electrode 97. As mentioned previously, the reservoir and pump may alternately be mounted in the 20 pacemaker device itself. In either instance, the genetic material is delivered under very minimal pressure from the reservoir through the lumen of the catheter to the electrode, where it is passed through the electrode central channel to contact myocardial cells. In yet another 25 embodiment, the lumen portion 87 provided by the cannula is utilized as the reservoir. In this embodiment, delivery may either be passive, or with the aid of a micropump (not shown). The genetic material can be preloaded into the cannula, or it can be inserted by a needle just before the 30 catheter is introduced and positioned with the patient.

In another embodiment, as illustrated in Figure 6B, a chamber 99 is provided just proximal from eluting electrode 97, and serves as the reservoir of the genetic material. Insulating material 96 is formed from a self- 35 sealing material such that it may be pierced with a needle, or the like, and reseal itself, thus allowing introduction of the genetic material into the chamber prior to

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implantation. Alternately, insulating material 96 can contain a port (not shown) through which the needle inserts the genetic material. In this embodiment, delivery of the material is without a pump, i.e., passive, the material 5 draining slowly through the microporous portion of electrode 97.

As used herein, the phrase "cardiac conduction disturbance" refers to disturbances or disruptions of the normal cardiac conduction system in a mammal. Such 10 disturbances may be the result of congenital phenomena or trauma, and can manifest in conditions such as, for example, sick sinus syndrome, "brady-tachy syndrome," heart block, bradycardia, tachycardia, and other arrhythmic conditions. Manifestations of such cardiac conduction disturbances have 15 been traditionally treated by drugs, artificial conduction systems such as pacemakers, ablation therapy, or a combination thereof.

As used herein, the phrase "conduction protein genetic material" refers to recombinant nucleic acid 20 molecules encoding the conduction proteins or, alternatively, the conduction proteins themselves, which are used in the methods and delivery systems of the invention. For chronic treatment, or long term treatment, the 25 conduction protein genetic material will be in the form of recombinant nucleic acid molecules encoding the conduction protein. In contrast, for acute treatment, or short term treatment, the conduction protein genetic material will be in the form of the conduction proteins themselves. Once the conduction protein genetic material has been selected, it is 30 referred to as "predetermined genetic material."

A "recombinant nucleic acid molecule", as used herein, is comprised of an isolated conduction protein-encoding nucleotide sequence inserted into a delivery vehicle. Regulatory elements, such as the promoter and 35 polyadenylation signal, are operably linked to the nucleotide sequence encoding the conduction protein, whereby

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the protein is capable of being produced when the recombinant nucleic acid molecule is introduced into a cell.

The nucleic acid molecules encoding the conduction proteins are prepared synthetically or, preferably, from isolated nucleic acid molecules, as described below. A nucleic acid is "isolated" when purified away from other cellular constituents, such as, for example, other cellular nucleic acids or proteins, by standard techniques known to those of ordinary skill in the art. The coding region of the nucleic acid molecule encoding the conduction protein can encode a full length gene product or a subfragment thereof, or a novel mutated or fusion sequence. The protein coding sequence can be a sequence endogenous to the target cell, or exogenous to the target cell. The promoter, with which the coding sequence is operably associated, may or may not be one that normally is associated with the coding sequence.

The nucleic acid molecule encoding the conduction protein is inserted into an appropriate delivery vehicle, such as, for example, an expression plasmid, cosmid, YAC vector, and the like. Almost any delivery vehicle can be used for introducing nucleic acids into the cardiovascular system, including, for example, recombinant vectors, such as one based on adenovirus serotype 5, Ad5, as set forth in French, et al., *Circulation*, 1994, 90, 2414-2424, which is incorporated herein by reference. An additional protocol for adenovirus-mediated gene transfer to cardiac cells is set forth in WO 94/11506 and in Barr, et al., *Gene Ther.*, 1994, 1, 51-58, both of which are incorporated herein by reference. Other recombinant vectors include, for example, plasmid DNA vectors, such as one derived from pGEM3 or pBR322, as set forth in Acsadi, et al., *The New Biol.*, 1991, 3, 71-81, and Gal, et al., *Lab. Invest.*, 1993, 68, 18-25, both of which are incorporated herein by reference, cDNA-containing liposomes, artificial viruses, nanoparticles, and the like. It is also contemplated that conduction proteins be injected directly into the myocardium.

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The regulatory elements of the recombinant nucleic acid molecules of the invention are capable of directing expression in mammalian cells, specifically human cells. The regulatory elements include a promoter and a

5 polyadenylation signal. In addition, other elements, such as a Kozak region, may also be included in the recombinant nucleic acid molecule. Examples of polyadenylation signals useful to practice the present invention include, but are not limited to, SV40 polyadenylation signals and LTR

10 polyadenylation signals. In particular, the SV40 polyadenylation signal which is in pCEP4 plasmid (Invitrogen, San Diego, CA), referred to as the SV40 polyadenylation signal, can be used.

The promoters useful in constructing the recombinant nucleic acid molecules of the invention may be constitutive or inducible. A constitutive promoter is expressed under all conditions of cell growth. Exemplary constitutive promoters include the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase,  $\beta$ -actin, human myosin, human hemoglobin, human muscle creatine, and others. In addition, many viral promoters function constitutively in eukaryotic cells, and include, but are not limited to, the early and late promoters of SV40, the Mouse Mammary Tumor Virus (MMTV) promoter, the long terminal repeats (LTRs) of Maloney leukemia virus, Human Immunodeficiency Virus (HIV), Cytomegalovirus (CMV) immediate early promoter, Epstein Barr Virus (EBV), Rous Sarcoma Virus (RSV), and other retroviruses, and the thymidine kinase promoter of herpes simplex virus. Other promoters are known to those of ordinary skill in the art.

Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein promoter is induced to promote (increase) transcription in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

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Promoters and polyadenylation signals used must be functional within the cells of the mammal. In order to maximize protein production, regulatory sequences may be selected which are well suited for gene expression in the 5 cardiac cells into which the recombinant nucleic acid molecule is administered. For example, the promoter is preferably a cardiac tissue-specific promoter-enhancer, such as, for example, cardiac isoform troponin C (cTNC) promoter. Parmacek, et al., *J. Biol. Chem.*, 1990, 265, 15970-15976, 10 and Parmacek, et al., *Mol. Cell Biol.*, 1992, 12, 1967-1976. In addition, codons may be selected which are most efficiently transcribed in the cell. One having ordinary skill in the art can produce recombinant nucleic acid molecules which are functional in the cardiac cells.

15 Genetic material can be introduced into a cell or "contacted" by a cell by, for example, transfection or transduction procedures. Transfection refers to the acquisition by a cell of new genetic material by incorporation of added nucleic acid molecules. Transfection 20 can occur by physical or chemical methods. Many transfection techniques are known to those of ordinary skill in the art including: calcium phosphate DNA co-precipitation; DEAE-dextran DNA transfection; electroporation; naked plasmid adsorption, and cationic 25 liposome-mediated transfection. Transduction refers to the process of transferring nucleic acid into a cell using a DNA or RNA virus. Suitable viral vectors for use as transducing agents include, but are not limited to, retroviral vectors, adeno associated viral vectors, vaccinia viruses, and 30 Semliki Forest virus vectors.

Treatment of cells, or contacting cells, with recombinant nucleic acid molecules can take place *in vivo* or *ex vivo*. For *ex vivo* treatment, cells are isolated from an animal (preferably a human), transformed (*i.e.*, transduced 35 or transfected *in vitro*) with a delivery vehicle containing a nucleic acid molecule encoding a conduction protein, and then administered to a recipient. Procedures for removing

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cells from mammals are well known to those of ordinary skill in the art. In addition to cells, tissue or the whole or parts of organs may be removed, treated *ex vivo* and then returned to the patient. Thus, cells, tissue or organs may 5 be cultured, bathed, perfused and the like under conditions for introducing the recombinant nucleic acid molecules of the invention into the desired cells.

For *in vivo* treatment, cells of an animal, preferably a mammal and most preferably a human, are 10 transformed *in vivo* with a recombinant nucleic acid molecule of the invention. The *in vivo* treatment may involve systemic intravenous treatment with a recombinant nucleic acid molecule, local internal treatment with a recombinant nucleic acid molecule, such as by localized perfusion or 15 topical treatment, and the like. When performing *in vivo* administration of the recombinant nucleic acid molecule, the preferred delivery vehicles are based on noncytopathic eukaryotic viruses in which nonessential or complementable genes have been replaced with the nucleic acid sequence of 20 interest. Such noncytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Retroviruses have recently been approved for human gene therapy trials. Most 25 useful are those retroviruses that are replication-deficient (*i.e.*, capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for high-efficiency 30 transduction of genes *in vivo*. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell line with plasmid, production of recombinant retroviruses by the packaging cell 35 line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M. "Gene Transfer and

Expression, a Laboratory Manual", W.H. Freeman Co., New York (1990) and Murry, E.J. e.d. "Methods in Molecular Biology", Vol. 7, Humana Press, Inc., Cliffton, New Jersey (1991).

A preferred virus for contacting cells in certain applications, such as in *in vivo* applications, is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus can be engineered to be replication deficient and is capable of infecting a wide range of cell types and species. It further has advantages such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hemopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. Recent reports indicate that the adeno-associated virus can also function in an extrachromosomal fashion.

In preferred embodiments of the present invention, the recombinant nucleic acid molecules comprising nucleic acid molecules encoding the conduction proteins, or, in the alternative, the conduction proteins, are delivered to the cardiac cells of the identified cardiac location, as determined by mapping procedures set forth above, using the delivery systems set forth above. Alternatively, the conduction protein genetic material is delivered to the cardiac cells of the identified cardiac location by direct injection.

In preferred embodiments of the present invention, the nucleic acid molecules encoding the conduction proteins comprise the full length coding sequence cDNA of a conduction protein. Preferably, the conduction proteins are the gap junction proteins; more preferably, they are the connexin proteins. Such nucleic acid molecules are described in the Fishman, et al., *J. Cell. Biol.*, 1990, 111, 589-598, and Kanter, et al., *J. Mol. Cell Cardiol.*, 1994, 26, 861-868 references, both of which are incorporated herein by reference, which contain the full length coding sequence cDNA of the connexin gap junction proteins Cx43, and Cx40 and Cx45, respectively.

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Introduction of the gap junction-encoding nucleic acid molecules or the gap junction proteins to normal cardiac cells surrounding a scar causing heart block will result in normal or enhanced conduction. Alternatively, it 5 is proposed that introduction of the gap junction-encoding nucleic acid molecules or the gap junction proteins to abnormal cardiac cells, those cells exhibiting cardiac conduction disturbances, will result in normal or enhanced conduction properties. Determining the appropriate 10 conduction protein genetic material, i.e., determining which connexin protein is appropriate, is dependent upon the particular cardiac conduction disturbance diagnosed. For example, if the cardiac conduction pathway disturbance is a heart block or bradycardia, in which conductance is slowed 15 or non-existent, Cx43 or Cx40, the faster connexins, is preferably used. However, if the cardiac conduction pathway disturbance is tachycardia, in which conductance is too rapid, Cx45 is preferably used.

Nucleic acid molecules comprising nucleotide 20 sequences encoding the connexin proteins Cx40, Cx43, and Cx45 are isolated and purified according to the methods set forth in Fishman, et al., *J. Cell. Biol.*, 1990, 111, 589-598, and Kanter, et al., *J. Mol. Cell Cardiol.*, 1994, 26, 861-868. The nucleic acid and protein sequences of Cx40 are 25 set forth in SEQ ID NO:1 and SEQ ID NO:2, respectively. The nucleic acid and protein sequences of Cx43 are set forth in SEQ ID NO:3 and SEQ ID NO:4, respectively. The nucleic acid and protein sequences of Cx45 are set forth in SEQ ID NO:5 and SEQ ID NO:6, respectively. It is contemplated that 30 nucleic acid molecules comprising nucleotide sequences that are preferably at least 70% homologous, more preferably at least 80% homologous, and most preferably at least 90% homologous to the connexin nucleotide sequences described in SEQ ID NOS 1, 3 and 5, can also be used.

35 It is understood that minor modifications of nucleotide sequence or the primary amino acid sequence may result in proteins which have substantially equivalent or

enhanced activity as compared to the conduction proteins exemplified herein. These modifications may be deliberate, as through site-directed mutagenesis, or may be accidental such as through mutations in hosts which produce the 5 conduction proteins. A "mutation" in a protein alters its primary structure (relative to the commonly occurring or specifically described protein) due to changes in the nucleotide sequence of the DNA which encodes it. These mutations specifically include allelic variants. Mutational 10 changes in the primary structure of a protein can result from deletions, additions, or substitutions. A "deletion" is defined as a polypeptide in which one or more internal amino acid residues are absent as compared to the native sequence. An "addition" is defined as a polypeptide which 15 has one or more additional internal amino acid residues as compared to the wild type protein. A "substitution" results from the replacement of one or more amino acid residues by other residues. A protein "fragment" is a polypeptide consisting of a primary amino acid sequence which is 20 identical to a portion of the primary sequence of the protein to which the polypeptide is related.

Preferred "substitutions" are those which are conservative, i.e., wherein a residue is replaced by another of the same general type. As is well understood, naturally- 25 occurring amino acids can be subclassified as acidic, basic, neutral and polar, or neutral and nonpolar and/or aromatic. It is generally preferred that encoded peptides differing from the native form contain substituted codons for amino acids which are from the same group as that of the amino 30 acid replaced. Thus, in general, the basic amino acids Lys, Arg, and Histidine are interchangeable; the acidic amino acids Asp and Glu are interchangeable; the neutral polar amino acids Ser, Thr, Cys, Gln, and Asn are interchangeable; the nonpolar aliphatic acids Gly, Ala, Val, Ile, and Leu are 35 conservative with respect to each other (but because of size, Gly and Ala are more closely related and Val, Ile and

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Leu are more closely related), and the aromatic amino acids Phe, Trp, and Tyr are interchangeable.

While Pro is a nonpolar neutral amino acid, it represents difficulties because of its effects on 5 conformation, and substitutions by or for Pro are not preferred, except when the same or similar conformational results can be obtained. Polar amino acids which represent conservative changes include Ser, Thr, Gln, Asn; and to a lesser extent, Met. In addition, although classified in 10 different categories, Ala, Gly, and Ser seem to be interchangeable, and Cys additionally fits into this group, or may be classified with the polar neutral amino acids. Some substitutions by codons for amino acids from different classes may also be useful.

Once the nucleic acid molecules encoding the connexin proteins are isolated and purified according to the methods described above, recombinant nucleic acid molecules are prepared in which the desired connexin nucleic acid molecule is incorporated into a delivery vehicle by methods 15 known to those skilled in the art, as taught in, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Ed. Cold Spring Harbor Press (1989). Preferred delivery vehicles include, for example, plasmids (Acsadi, et al., *The New Biol.*, 1991, 3, 71-81, and Gal, et 20 al., *Lab. Invest.*, 1993, 68, 18-25, both of which are incorporated herein by reference) and adenovirus (WO 94/11506 and in Barr, et al., *Gene Ther.*, 1994, 1, 51-58, both of which are incorporated herein by reference). The nucleic acid molecules encoding connexin proteins, or 25 connexin proteins produced therefrom, are delivered to the cardiac cells of the identified cardiac location by the delivery systems of the present invention. Thus, such delivery systems of the present invention are used to contact the cardiac cells of the identified cardiac 30 location, which comprises cardiac cells having cardiac conduction disturbances, with recombinant nucleic acid molecules encoding a connexin protein, or connexin proteins.

Where the conduction protein genetic material is in the form of conduction proteins, such proteins can be prepared in large quantities by using various standard expression systems known to those skilled in the art.

- 5 Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Ed. Cold Spring Harbor Press (1989), pp. 16.1-16.55, incorporated herein by reference.

The recombinant nucleic acid molecules or connexin proteins are preferably delivered in a pharmaceutical composition. Such pharmaceutical compositions can include, for example, the recombinant nucleic acid molecule or protein in a volume of phosphate-buffered saline with 5% sucrose. In other embodiments of the invention, the recombinant nucleic acid molecule or protein is delivered with suitable pharmaceutical carriers, such as those described in the most recent edition of *Remington's Pharmaceutical Sciences*, A. Osol, a standard reference text in this field. The recombinant nucleic acid molecule or protein is delivered in a therapeutically effective amount. Such amount is determined experimentally and is that amount which either restores normal conduction or improves abnormal conduction of cardiac cells. The amount of recombinant nucleic acid molecule or protein is preferably between 0.01 µg and 100 mg, more preferably between 0.1 µg and 10 mg, more preferably between 1 µg and 1 mg, and most preferably between 10 µg and 1 mg. A single therapeutically effective amount is referred to as a bolus. Where adenovirus vectors are used, the amount of recombinant nucleic acid molecule is preferably between  $10^7$  plaque forming units (pfu) and  $10^{15}$  pfu, more preferably between  $10^8$  pfu and  $10^{14}$  pfu, and most preferably between  $10^9$  pfu and  $10^{12}$  pfu. A single therapeutically effective amount of conduction protein genetic material is referred to as a bolus. In some embodiments of the present invention, the delivery of the recombinant nucleic acid molecules or proteins is combined with steroid elution, such as with dexamethasone sodium

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phosphate, beclamethasone, and the like, to control inflammatory processes.

The following examples are meant to be exemplary of the preferred embodiments of the invention and are not 5 meant to be limiting.

#### EXAMPLES

##### Example 1: Isolation and Purification of Nucleic Acid Molecules Encoding the Connexin Proteins

Nucleic acid molecules encoding Cx43, Cx40, and 10 Cx45 are isolated and purified according to general methods well known to those skilled in the art. Briefly, total cellular RNA is isolated and purified (Chomczynsky, et al., *Anal. Biochem.*, 1987, 162, 156-159) from heart tissue, cardiac transplantation donors, or from salvaged tissue, and 15 selected for poly(A) RNA (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Ed. Cold Spring Harbor Press (1989), pp. 7.26-7.29). cDNA corresponding to the connexin proteins is prepared from the poly(A) cardiac RNA by reverse transcription using a GENEAMP™ PCR kit (Perkin 20 Elmer Cetus, Norwalk, CT), or the like, using random hexamers according to the manufacturer's instructions. The specific connexin nucleic acid molecules are amplified by the polymerase chain reaction (PCR), also using the GENEAMP™ PCR kit, or the like, using forward and reverse primers 25 specific for each of the different connexin proteins, according to the manufacturer's instructions. For example, the forward primer for Cx43 can be 5'- ATGCCTGACTGGACCAGCCTTAGGC-3' (SEQ ID NO:7), and the reverse primer can be 5'-GATCTCGAGGTCATCAGGCCGAGG-3' (SEQ ID NO:8). 30 For example, the forward primer for Cx45 can be 5'- ATGAGTTGGAGCTTCTGACTCGC-3' (SEQ ID NO:9), and the reverse primer can be 5'-AATCCAGACAGAGTTCTCCCATC-3' (SEQ ID NO:10). For example, the forward primer for Cx40 can be 5'- ATGGGCGATTGGAGCTTCCTGGGA-3' (SEQ ID NO:11), and the reverse 35 primer can be 5'-CACTGATAGGTCACTGACCTTGC-3' (SEQ ID NO:12). It is understood that additional primers can be used for amplification as determined by those skilled in the art.

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These primers may be preceded at the 5' terminus by nucleotide sequences containing endonuclease restriction sites for easy incorporation into vectors. The specific connexin nucleic acid molecules can also be amplified by PCR from human genomic DNA (Stratagene, San Diego, CA). After cutting the PCR products with the appropriate restriction endonuclease(s), the PCR products are purified by phenol:chloroform extractions, or using commercial purification kits, such as, for example, MAGIC™ Minipreps DNA Purification System (Promega, Madison, WI). The specific nucleotide sequence of the PCR products is determined by conventional DNA sequencing procedures, and the identity of the PCR products confirmed by comparison to the published sequences for the connexin proteins.

15 **Example 2: Insertion of Connexin cDNA into Delivery Vehicles**

Preferably, connexin cDNA is inserted into either plasmid or adenoviral vectors. Plasmid vectors include for example, pGEM3 or pBR322, as set forth in Acsadi, et al., *The New Biol.*, 1991, 3, 71-81, and Gal, et al., *Lab. Invest.*, 1993, 68, 18-25. Adenoviral vectors include for example, adenovirus serotype 5, Ad5, as set forth in French, et al., *Circulation*, 1994, 90, 2414-2424.

Preferably, the primers used to amplify the connexin nucleic acid molecules are designed with unique 25 endonuclease restriction sites located at the 5' terminus. In the absence of such design, polylinker arms, containing unique restriction sites, can be ligated thereto. After cutting the purified PCR products with the appropriate restriction endonuclease(s), the plasmid vector, comprising 30 a polylinker, is also cut with the same restriction endonuclease(s), affording the connexin nucleic acid molecule a site at which to ligate. In a similar manner, recombinant adenovirus (Gluzman, et al., in *Eukaryotic Viral Vectors*, Gluzman, ed., Cold Spring Harbor Press, 1982, 35 pp.187-192, and French, et al., *Circulation*, 1994, 90, 2414-2424) containing connexin cDNA molecules are prepared in

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accordance with standard techniques well known to those skilled in the art.

It is contemplated that variations of the above-described invention may be constructed that are consistent  
5 with the spirit of the invention.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Stokes, Kenneth  
Morissette, Josée
- (ii) TITLE OF INVENTION: SYSTEM FOR GENETICALLY TREATING CARDIAC CONDUCTION DISTURBANCES
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris LLP
  - (B) STREET: One Liberty Place - 46th Floor
  - (C) CITY: Philadelphia
  - (D) STATE: PA
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: WordPerfect 6.1
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: N/A
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Paul K. Legaard
  - (B) REGISTRATION NUMBER: 38,534
  - (C) REFERENCE/DOCKET NUMBER: MEDT-0059
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (215) 568-3100
  - (B) TELEFAX: (215) 568-3439
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1074 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GGC GAT TGG AGC TTC CTG GGA AAT TTC CTG GAG GAA GTA CAC	45
Met Gly Asp Trp Ser Phe Leu Gly Asn Phe Leu Glu Glu Val His	
1 5 10 15	
AAG CAC TCG ACC GTG GTA GGC AAG GTC TGG CTC ACT GTC CTC TTC	90
Lys His Ser Thr Val Val Gly Lys Val Trp Leu Thr Val Leu Phe	
20 25 30	
ATA TTC CGT ATG CTC GTG CTG GGC ACA GCT GCT GAG TCT ACC TGG	135
Ile Phe Arg Met Leu Val Leu Gly Thr Ala Ala Glu Ser Thr Trp	
35 40 45	
GGG GAT GAG CAG GCT GAT TTC CGG TGT GAT ACG ATT CAG CCT GGC	180
Gly Asp Glu Gln Ala Asp Phe Arg Cys Asp Thr Ile Gln Pro Gly	
50 55 60	
TGC CAC AAT GTC TGC TAC GAC CAG GCT TTC CCC ATC TCC CAC ATT	225
Cys His Asn Val Cys Tyr Asp Gln Ala Phe Pro Ala Ser His Ile	
65 70 75	

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CGC TAC TGG GTG CTG CAG ATC ATC TTC GTC TCT ACG CCC TCT CTG Arg Tyr Trp Val Leu Gln Ile Ile Phe Val Ser Thr Pro Ser Leu 80 85 90	270
GTG TAC ATG GGC CAC GCC ATG CAC ACT GTG CGC ATG CAG GAG AAG Val Tyr Met Gly His Ala Met His Thr Val Arg Met Gln Glu Lys 95 100 105	315
CGC AAG CTA CGG GAG GCC GAG AGG GCC AAA GAG GTC CGG GGC TCT Arg Lys Leu Arg Glu Ala Glu Arg Ala Lys Glu Val Arg Gly Ser 110 115 120	360
GCC TCT TAC GAG TAC CCG GTG GCA GAG AAG GCA GAA CTG TCC TGC Gly Ser Tyr Glu Pro Val Ala Glu Lys Ala Glu Leu Ser Cys 125 130 135	405
TGG GAG GAA GGG AAT GGA AGG ATT GCC CTC CAG GGC ACT CTG CTC Trp Glu Glu Asn Gly Arg Ile Ala Leu Gln Gly Thr Leu Leu 140 145 150	450
AAC ACC TAT GTG TGC AGC ATC CTG ATC CGC ACC ACC ATG GAG GTG Asn Thr Tyr Val Cys Ser Ile Leu Ile Arg Thr Thr Met Glu Val 155 160 165	495
GGC TTC ATT GTG GGC CAG TAC TTC ATC TAC GGA ATC TTC CTG ACC Gly Phe Ile Val Gly Gln Tyr Phe Ile Tyr Gly Ile Phe Leu Thr 170 175 180	540
ACC CTG CAT GTC TGC CGC AGG AGT CCC TGT CCC CAC CCG GTC AAC Thr Leu His Val Cys Arg Arg Ser Pro Cys Pro His Pro Val Asn 185 190 195	585
TGT TAC GTA TCC CGG CCC ACA GAG AAG AAT GTC TTC ATT GTC TTT Cys Tyr Val Ser Arg Pro Thr Glu Lys Asn Val Phe Ile Val Phe 200 205 210	630
ATG CTG GCT GTG GCT GCA CTG TCC CTC CTC CTT AGC CTG GCT GAA Met Leu Ala Val Ala Ala Leu Ser Leu Leu Ser Leu Ala Glu 215 220 225	675
CTC TAC CAC CTG GGC TGG AAG AAG ATC AGA CAG CGA TTT GTC AAA Leu Tyr His Leu Gly Trp Lys Lys Ile Arg Gln Arg Phe Val Lys 230 235 240	720
CCG CGG CAG TAC ATG GCT AAG TGC CAG CTT TCT GGC CCT CTG TGG Pro Arg Gln Trp Met Ala Lys Cys Gln Leu Ser Gly Pro Leu Trp 245 250 255	765
GCT ATA GTC CAG AGC TGC ACA CCA CCC CCC GAC TTT AAT CAG TGC Ala Ile Val Gln Ser Cys Thr Pro Pro Asp Phe Asn Gln Cys 260 265 270	810
CTG GAG AAT GGT CCT GGG GGA AAA TTC TTC AAT CCC TTC AGC AAT Leu Glu Asn Gly Pro Gly Gly Lys Phe Phe Asn Pro Phe Ser Asn 275 280 285	855
AAT ATG GCC TCC CAA CAA AAC ACA GAC AAC CTG GTC ACC GAG CAA Asn Met Ala Ser Gln Gln Asn Thr Asp Asn Leu Val Thr Glu Gln 290 295 300	900
GTA CGA GGT CAG GAG CAG ACT CCT GGG GAA GGT TTC ATC CAG GTT Val Arg Gly Gln Glu Gln Thr Pro Gly Glu Gly Phe Ile Gln Val 305 310 315	945

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CGT TAT GGC CAG AAG CCT GAG GTG CCC AAT GGA GTC TCA CCA GGT	990
Arg Tyr Gly Gln Lys Pro Glu Val Pro Asn Gly Val Ser Pro Gly	
320	325
	330
CAC CGC CTT CCC CAT GGC TAT CAT AGT GAC AAG CGA CGT CTT AGT	1035
His Arg Leu Pro His Gly Tyr His Ser Asp Lys Arg Arg Leu Ser	
335	340
	345
AAG GCC AGC AGC AAG GCA AGG TCA GAT GAC CTA TCA GTG	1074
Lys Ala Ser Ser Lys Ala Arg Ser Asp Asp Leu Ser Val	
350	355

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Asp Trp Ser Phe Leu Gly Asn Phe Leu Glu Glu Val His			
1	5	10	15
Lys His Ser Thr Val Val Gly Lys Val Trp Leu Thr Val Leu Phe			
20		25	30
Ile Phe Arg Met Leu Val Leu Gly Thr Ala Ala Glu Ser Thr Trp			
35		40	45
Gly Asp Glu Gln Ala Asp Phe Arg Cys Asp Thr Ile Gln Pro Gly			
50		55	60
Cys His Asn Val Cys Tyr Asp Gln Ala Phe Pro Ala Ser His Ile			
65		70	75
Arg Tyr Trp Val Leu Gln Ile Ile Phe Val Ser Thr Pro Ser Leu			
80		85	90
Val Tyr Met Gly His Ala Met His Thr Val Arg Met Gln Glu Lys			
95		100	105
Arg Lys Leu Arg Glu Ala Glu Arg Ala Lys Glu Val Arg Gly Ser			
110		115	120
Gly Ser Tyr Glu Tyr Pro Val Ala Glu Lys Ala Glu Leu Ser Cys			
125		130	135
Trp Glu Glu Glu Asn Gly Arg Ile Ala Leu Gln Gly Thr Leu Leu			
140		145	150
Asn Thr Tyr Val Cys Ser Ile Leu Ile Arg Thr Thr Met Glu Val			
155		160	165
Gly Phe Ile Val Gly Gln Tyr Phe Ile Tyr Gly Ile Phe Leu Thr			
170		175	180
Thr Leu His Val Cys Arg Arg Ser Pro Cys Pro His Pro Val Asn			
185		190	195
Cys Tyr Val Ser Arg Pro Thr Glu Lys Asn Val Phe Ile Val Phe			
200		205	210
Met Leu Ala Val Ala Ala Leu Ser Leu Leu Leu Ser Leu Ala Glu			
215		220	225
Leu Tyr His Leu Gly Trp Lys Lys Ile Arg Gln Arg Phe Val Lys			
230		235	240

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Pro	Arg	Gln	Trp	Met	Ala	Lys	Cys	Gln	Leu	Ser	Gly	Pro	Leu	Trp
245														255
Ala	Ile	Val	Gln	Ser	Cys	Thr	Pro	Pro	Pro	Asp	Phe	Asn	Gln	Cys
	260									265			270	
Leu	Glu	Asn	Gly	Pro	Gly	Gly	Lys	Phe	Phe	Asn	Pro	Phe	Ser	Asn
		275						280					285	
Asn	Met	Ala	Ser	Gln	Gln	Asn	Thr	Asp	Asn	Leu	Val	Thr	Glu	Gln
	290							295					300	
Val	Arg	Gly	Gln	Glu	Gln	Thr	Pro	Gly	Glu	Gly	Phe	Ile	Gln	Val
		305							310				315	
Arg	Tyr	Gly	Gln	Lys	Pro	Glu	Val	Pro	Asn	Gly	Val	Ser	Pro	Gly
		320							325				330	
His	Arg	Leu	Pro	His	Gly	Tyr	His	Ser	Asp	Lys	Arg	Arg	Leu	Ser
		335							340				345	
Lys	Ala	Ser	Ser	Lys	Ala	Arg	Ser	Asp	Asp	Leu	Ser	Val		
		350							355					

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	GGT	GAC	TGG	AGC	GCC	TTA	GGC	AAA	CTC	CTT	GAC	AAG	GTT	CAA	45
Met															
1						5				10					15
Gly	Asp	Trp	Ser	Ala	Leu	Gly	Lys		Leu	Leu	Asp	Lys	Val	Gln	
GCC	TAC	TCA	ACT	GCT	GGA	GGG	AAG	GTG	TGG	CTG	TCA	GTA	CTT	TTC	90
Ala	Tyr	Ser	Thr	Ala	Gly	Gly	Lys	Val	Trp	Leu	Ser	Val	Leu	Phe	
									20	25				30	
ATT	TTC	CGA	ATC	CTG	CTG	CTG	GGG	ACA	GCG	GTT	GAG	TCA	GCC	TGG	135
Ile	Phe	Arg	Ile	Leu	Leu	Leu	Gly	Thr	Ala	Val	Glu	Ser	Ala	Trp	
									35	40				45	
GGA	GAT	GAG	CAG	TCT	GCC	TTT	CGT	TGT	AAC	ACT	CAG	CAA	CCT	GGT	180
Gly	Asp	Glu	Gln	Ser	Ala	Phe	Arg	Cys	Asn	Thr	Gln	Gln	Pro	Gly	
						50				55				60	
TGT	GAA	AAT	GTC	TGC	TAT	GAC	AAG	TCT	TTC	CCA	ATC	TCT	CAT	GTG	225
Cys	Glu	Asn	Val	Cys	Tyr	Asp	Lys	Ser	Phe	Pro	Ile	Ser	His	Val	
						65			70				75		
CGC	TTC	TGG	GTC	CTG	CAG	ATC	ATA	TTT	GTG	TCT	GTA	CCC	ACA	CTC	270
Arg	Phe	Trp	Val	Leu	Gln	Ile	Ile	Phe	Val	Ser	Val	Pro	Thr	Leu	
								80		85				90	
TTG	TAC	CTG	GCT	CAT	GTG	TTC	TAT	GTG	ATG	CGA	AAG	GAA	GAG	AAA	315
Leu	Tyr	Leu	Ala	His	Val	Phe	Tyr	Val	Met	Arg	Lys	Glu	Glu	Lys	
						95				100				105	
CTG	AAC	AAG	AAA	GAG	GAA	GAA	CTC	AAG	GTT	GCC	CAA	ACT	GAT	GGT	360
Leu	Asn	Lys	Lys	Glu	Glu	Glu	Leu	Lys	Val	Ala	Gln	Thr	Asp	Gly	
							110			115				120	
GTC	AAT	GTG	GAC	ATG	CAC	TTG	AAG	CAG	ATT	GAG	ATA	AAG	AAG	TTC	405
Val	Asn	Val	Asp	Met	His	Leu	Lys	Gln	Ile	Glu	Ile	Lys	Lys	Phe	
						125			130				135		

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AAG TAC GGT ATT GAA GAG CAT GGT AAG GTG AAA ATG CGA GGG GGG	450																																																																																																																																
Lys Tyr Gly Ile Glu Glu His Gly Lys Val Lys Met Arg Gly Gly																																																																																																																																	
140	145	150		TTG CTG CGA ACC TAC ATC ATC AGT ATC CTC TTC AAG TCT ATC TTT	495	Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe		155	160	165		GAG GTG GCC TTC TTG CTG ATC CAG TGG TAC ATC TAT GGA TTC AGC	540	Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile Tyr Gly Phe Ser		170	175	180		TTG AGT GCT GTT TAC ACT TGC AAA AGA GAT CCC TGC CCA CAT CAG	585	Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys Pro His Gln		185	190	195		GTG GAC TGT TTC CTC TCT CGC CCC ACG GAG AAA ACC ATC TTC ATC	630	Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile Phe Ile		200	205	210		ATC TTC ATG CTG GTG TCC TTG GTG TCC CTG GCC TTG AAT ATC	675	Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn Ile		215	220	225		ATT GAA CTC TTC TAT GTT TTC TTC AAG GGC GTT AAG GAT CGG GTT	720	Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		230	235	240		AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765	Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser		245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380	
150																																																																																																																																	
TTG CTG CGA ACC TAC ATC ATC AGT ATC CTC TTC AAG TCT ATC TTT	495																																																																																																																																
Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe																																																																																																																																	
155	160	165		GAG GTG GCC TTC TTG CTG ATC CAG TGG TAC ATC TAT GGA TTC AGC	540	Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile Tyr Gly Phe Ser		170	175	180		TTG AGT GCT GTT TAC ACT TGC AAA AGA GAT CCC TGC CCA CAT CAG	585	Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys Pro His Gln		185	190	195		GTG GAC TGT TTC CTC TCT CGC CCC ACG GAG AAA ACC ATC TTC ATC	630	Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile Phe Ile		200	205	210		ATC TTC ATG CTG GTG TCC TTG GTG TCC CTG GCC TTG AAT ATC	675	Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn Ile		215	220	225		ATT GAA CTC TTC TAT GTT TTC TTC AAG GGC GTT AAG GAT CGG GTT	720	Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		230	235	240		AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765	Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser		245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380									
165																																																																																																																																	
GAG GTG GCC TTC TTG CTG ATC CAG TGG TAC ATC TAT GGA TTC AGC	540																																																																																																																																
Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile Tyr Gly Phe Ser																																																																																																																																	
170	175	180		TTG AGT GCT GTT TAC ACT TGC AAA AGA GAT CCC TGC CCA CAT CAG	585	Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys Pro His Gln		185	190	195		GTG GAC TGT TTC CTC TCT CGC CCC ACG GAG AAA ACC ATC TTC ATC	630	Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile Phe Ile		200	205	210		ATC TTC ATG CTG GTG TCC TTG GTG TCC CTG GCC TTG AAT ATC	675	Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn Ile		215	220	225		ATT GAA CTC TTC TAT GTT TTC TTC AAG GGC GTT AAG GAT CGG GTT	720	Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		230	235	240		AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765	Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser		245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																	
180																																																																																																																																	
TTG AGT GCT GTT TAC ACT TGC AAA AGA GAT CCC TGC CCA CAT CAG	585																																																																																																																																
Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys Pro His Gln																																																																																																																																	
185	190	195		GTG GAC TGT TTC CTC TCT CGC CCC ACG GAG AAA ACC ATC TTC ATC	630	Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile Phe Ile		200	205	210		ATC TTC ATG CTG GTG TCC TTG GTG TCC CTG GCC TTG AAT ATC	675	Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn Ile		215	220	225		ATT GAA CTC TTC TAT GTT TTC TTC AAG GGC GTT AAG GAT CGG GTT	720	Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		230	235	240		AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765	Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser		245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																									
195																																																																																																																																	
GTG GAC TGT TTC CTC TCT CGC CCC ACG GAG AAA ACC ATC TTC ATC	630																																																																																																																																
Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile Phe Ile																																																																																																																																	
200	205	210		ATC TTC ATG CTG GTG TCC TTG GTG TCC CTG GCC TTG AAT ATC	675	Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn Ile		215	220	225		ATT GAA CTC TTC TAT GTT TTC TTC AAG GGC GTT AAG GAT CGG GTT	720	Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		230	235	240		AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765	Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser		245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																	
210																																																																																																																																	
ATC TTC ATG CTG GTG TCC TTG GTG TCC CTG GCC TTG AAT ATC	675																																																																																																																																
Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn Ile																																																																																																																																	
215	220	225		ATT GAA CTC TTC TAT GTT TTC TTC AAG GGC GTT AAG GAT CGG GTT	720	Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		230	235	240		AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765	Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser		245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																									
225																																																																																																																																	
ATT GAA CTC TTC TAT GTT TTC TTC AAG GGC GTT AAG GAT CGG GTT	720																																																																																																																																
Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val																																																																																																																																	
230	235	240		AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765	Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser		245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																	
240																																																																																																																																	
AAG GGA AAG AGC GAC CCT TAC CAT GCG ACC AGT GGT GCG CTG AGC	765																																																																																																																																
Lys Gly Lys Cys Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser																																																																																																																																	
245	250	255		CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810	Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly		260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																									
255																																																																																																																																	
CCT GCC AAA GAC TGT GGG TCT CAA AAA TAT GCT TAT TTC AAT GGC	810																																																																																																																																
Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly																																																																																																																																	
260	265	270		TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855	Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly		275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																	
270																																																																																																																																	
TGC TCC TCA CCA ACC GCT CCC CTC TCG CCT ATG TCT CCT CCT GGG	855																																																																																																																																
Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly																																																																																																																																	
275	280	285		TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900	Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn		290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																									
285																																																																																																																																	
TAC AAG CTG GTT ACT GGC GAC AGA AAC AAT TCT TCT TGC CGC AAT	900																																																																																																																																
Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn																																																																																																																																	
290	295	300		TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945	Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala		305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																																	
300																																																																																																																																	
TAC AAC AAG CAA GCA AGT GAG CAA AAC TGG GCT AAT TAC AGT GCA	945																																																																																																																																
Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala																																																																																																																																	
305	310	315		GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990	Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser		320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																																									
315																																																																																																																																	
GAA CAA AAT CGA ATG GGG CAG GCG GGA AGC ACC ATC TCT AAC TCC	990																																																																																																																																
Glu Gln Asn Arg Met Gly Gly Ala Gly Ser Thr Ile Ser Asn Ser																																																																																																																																	
320	325	330		CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035	His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys		335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																																																	
330																																																																																																																																	
CAT GCA CAG CCT TTT GAT TTC CCC GAT GAT AAC CAG AAT TCT AAA	1035																																																																																																																																
His Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys																																																																																																																																	
335	340	345		AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080	Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp		350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																																																									
345																																																																																																																																	
AAA CTA GCT GCT GGA CAT GAA TTA CAG CCA CTA GCC ATT GTG GAC	1080																																																																																																																																
Lys Leu Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp																																																																																																																																	
350	355	360		CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125	Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro		365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																																																																	
360																																																																																																																																	
CAG CGA CCT TCA AGC AGA GCC AGC AGT CGT GCC AGC AGC AGA CCT	1125																																																																																																																																
Gln Arg Pro Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro																																																																																																																																	
365	370	375		CGG CCT GAT GAC CTG GAG ATC	1146	Arg Pro Asp Asp Leu Glu Ile		380																																																																																																																									
375																																																																																																																																	
CGG CCT GAT GAC CTG GAG ATC	1146																																																																																																																																
Arg Pro Asp Asp Leu Glu Ile																																																																																																																																	
380																																																																																																																																	

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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Asp	Trp	Ser	Ala	Leu	Gly	Lys	Leu	Leu	Asp	Lys	Val	Gln
1					5				10				15	
Ala	Tyr	Ser	Thr	Ala	Gly	Gly	Lys	Val	Trp	Leu	Ser	Val	Leu	Phe
					20				25				30	
Ile	Phe	Arg	Ile	Leu	Leu	Gly	Thr	Ala	Val	Glu	Ser	Ala	Trp	
				35				40				45		
Gly	Asp	Glu	Gln	Ser	Ala	Phe	Arg	Cys	Asn	Thr	Gln	Gln	Pro	Gly
				50				55				60		
Cys	Glu	Asn	Val	Cys	Tyr	Asp	Lys	Ser	Phe	Pro	Ile	Ser	His	Val
				65				70				75		
Arg	Phe	Trp	Val	Leu	Gln	Ile	Ile	Phe	Val	Ser	Val	Pro	Thr	Leu
				80				85				90		
Leu	Tyr	Leu	Ala	His	Val	Phe	Tyr	Val	Met	Arg	Lys	Glu	Glu	Lys
				95				100				105		
Leu	Asn	Lys	Gly	Glu	Glu	Leu	Lys	Val	Ala	Gln	Thr	Asp	Gly	
				110				115				120		
Val	Asn	Val	Asp	Met	His	Leu	Lys	Gln	Ile	Glu	Ile	Lys	Lys	Phe
				125				130				135		
Lys	Tyr	Gly	Ile	Glu	Glu	His	Gly	Lys	Val	Lys	Met	Arg	Gly	Gly
				140				145				150		
Leu	Leu	Arg	Thr	Tyr	Ile	Ile	Ser	Ile	Leu	Phe	Lys	Ser	Ile	Phe
				155				160				165		
Glu	Val	Ala	Phe	Leu	Leu	Ile	Gln	Trp	Tyr	Ile	Tyr	Gly	Phe	Ser
				170				175				180		
Leu	Ser	Ala	Val	Tyr	Thr	Cys	Lys	Arg	Asp	Pro	Cys	Pro	His	Gln
				185				190				195		
Val	Asp	Cys	Phe	Leu	Ser	Arg	Pro	Thr	Glu	Lys	Thr	Ile	Phe	Ile
				200				205				210		
Ile	Phe	Met	Leu	Val	Val	Ser	Leu	Val	Ser	Leu	Ala	Leu	Asn	Ile
				215				220				225		
Ile	Glu	Leu	Phe	Tyr	Val	Phe	Phe	Lys	Gly	Val	Lys	Asp	Arg	Val
				230				235				240		
Lys	Gly	Lys	Cys	Asp	Pro	Tyr	His	Ala	Thr	Ser	Gly	Ala	Leu	Ser
				245				250				255		
Pro	Ala	Lys	Asp	Cys	Gly	Ser	Gln	Lys	Tyr	Ala	Tyr	Phe	Asn	Gly
				260				265				270		
Cys	Ser	Ser	Pro	Thr	Ala	Pro	Leu	Ser	Pro	Met	Ser	Pro	Pro	Gly
				275				280				285		

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Tyr	Lys	Leu	Val	Thr	Gly	Asp	Arg	Asn	Asn	Ser	Ser	Cys	Arg	Asn
								290	295				300	
Tyr	Asn	Lys	Gln	Ala	Ser	Glu	Gln	Asn	Trp	Ala	Asn	Tyr	Ser	Ala
								305	310			315		
Glu	Gln	Asn	Arg	Met	Gly	Gly	Ala	Gly	Ser	Thr	Ile	Ser	Asn	Ser
				320				325			330			
His	Ala	Gln	Pro	Phe	Asp	Phe	Pro	Asp	Asp	Asn	Gln	Asn	Ser	Lys
				335				340			345			
Lys	Leu	Ala	Ala	Gly	His	Glu	Leu	Gln	Pro	Leu	Ala	Ile	Val	Asp
				350				355			360			
Gln	Arg	Pro	Ser	Ser	Arg	Ala	Ser	Ser	Arg	Ala	Ser	Ser	Arg	Pro
				365				370			375			
Arg	Pro	Asp	Asp	Leu	Glu	Ile								
				380										

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG	AGT	TGG	AGC	TTT	CTG	ACT	CGC	CTG	CTA	GAG	GAG	ATT	CAC	AAC	45
Met	Ser	Trp	Ser	Phe	Leu	Thr	Arg	Leu	Leu	Glu	Glu	Ile	His	Asn	
1				5					10				15		
CAT	TCC	ACA	TTT	GTG	GGG	AAG	ATC	TGG	CTC	ACT	GTT	CTG	ATT	GTC	90
His	Ser	Thr	Phe	Val	Gly	Lys	Ile	Trp	Leu	Thr	Val	Leu	Ile	Val	
				20					25				30		
TTC	CGG	ATC	GTC	CTT	ACA	GCT	GTA	GGA	GGA	GAA	TCC	ATC	TAT	TAC	135
Phe	Arg	Ile	Val	Leu	Thr	Ala	Val	Gly	Gly	Glu	Ser	Ile	Tyr	Tyr	
				35				40				45			
GAT	GAG	CAA	AGC	AAA	TTT	GTG	TGC	AAC	ACA	GAA	CAG	CCG	GGC	TGT	180
Asp	Glu	Gln	Ser	Lys	Phe	Val	Cys	Asn	Thr	Glu	Gln	Pro	Gly	Cys	
				50				55				60			
GAG	AAT	GTC	TGT	TAT	GAT	GCG	TTT	GCA	CCT	CTC	TCC	CAT	GTA	CGC	225
Glu	Asn	Val	Cys	Tyr	Asp	Ala	Phe	Ala	Pro	Leu	Ser	His	Val	Arg	
				65				70				75			
TTC	TGG	GTG	TTC	CAG	ATC	ATC	CTG	GTG	GCA	ACT	CCC	TCT	GTG	ATG	270
Phe	Trp	Val	Phe	Gln	Ile	Ile	Leu	Val	Ala	Thr	Pro	Ser	Val	Met	
				80				85				90			
TAC	CTG	GGC	TAT	GCT	ATC	CAC	AAG	ATT	GCC	AAA	ATG	GAG	CAC	GGT	315
Tyr	Leu	Gly	Tyr	Ala	Ile	His	Lys	Ile	Ala	Lys	Met	Glu	His	Gly	
				95				100				105			
GAA	GCA	GAC	AAG	AAG	GCA	GCT	CGG	AGC	AAG	CCC	TAT	GCA	ATG	CGC	360
Glu	Ala	Asp	Lys	Lys	Ala	Ala	Arg	Ser	Lys	Pro	Tyr	Ala	Met	Arg	
				110				115				120			
TGG	AAA	CAA	CAC	CGG	GCT	CTG	GAA	GAA	ACG	GAG	GAG	GAC	AAC	GAA	405
Trp	Lys	Gln	His	Arg	Ala	Leu	Glu	Glu	Thr	Glu	Glu	Asp	Asn	Glu	
				125				130				135			

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GAG GAT CCT ATG ATG TAT CCA GAG ATG GAG TTA GAA AGT GAT AAG Glu Asp Pro Met Met Tyr Pro Glu Met Glu Leu Glu Ser Asp Lys 140 145 150	450
GAA AAT AAA GAG CAG AGC CAA CCC AAA CCT AAG CAT GAT GGC CGA Glu Asn Lys Glu Gln Ser Gln Pro Lys Pro Lys His Asp Gly Arg 155 160 165	495
CGA CGG ATT CGG GAA GAT GGG CTC ATG AAA ATC TAT GTG CTG CAG Arg Arg Ile Arg Glu Asp Gly Leu Met Lys Ile Tyr Val Leu Gln 170 175 180	540
TTG CTG GCA AGG ACC GTG TTT GAG GTG GGT TTT CTG ATA GGG CAG Leu Leu Ala Arg Thr Val Phe Glu Val Gly Phe Leu Ile Gly Gln 185 190 195	585
TAT TTT CTG TAT GGC TTC CAA GTC CAC CCG TTT TAT GTG TGC AGC Tyr Phe Leu Tyr Gly Phe Gln Val His Pro Phe Tyr Val Cys Ser 200 205 210	630
AGA CTT CCT TGT CCT CAT AAG ATA GAC TGC TTT ATT TCT AGA CCC Arg Leu Pro Cys Pro His Lys Ile Asp Cys Phe Ile Ser Arg Pro 215 220 225	675
ACT GAA AAG ACC ATC TTC CTT CTG ATA ATG TAT GGT GTT ACA GGC Thr Glu Lys Thr Ile Phe Leu Leu Ile Met Tyr Gly Val Thr Gly 230 235 240	720
CTT TGC CTC TTG CTT AAC ATT TGG GAG ATG CTT CAT TTA GGG TTT Leu Cys Leu Leu Leu Asn Ile Trp Glu Met Leu His Leu Gly Phe 245 250 255	765
GGG ACC ATT CGA GAC TCA CTA AAC AGT AAA AGG AGG GAA CTT GAG Gly Thr Ile Arg Asp Ser Leu Asn Ser Lys Arg Arg Glu Leu Glu 260 265 270	810
GAT CCG GGT GCT TAT AAT TAT CCT TTC ACT TGG AAT ACA CCA TCT Asp Pro Gly Ala Tyr Asn Tyr Pro Phe Thr Trp Asn Thr Pro Ser 275 280 285	855
GCT CCC CCT GGC TAT AAC ATT GCT GTC AAA CCA GAT CAA ATC CAG Ala Pro Pro Gly Tyr Asn Ile Ala Val Lys Pro Asp Gln Ile Gln 290 295 300	900
TAC ACC GAA CTG TCC AAT GCT AAG ATC GCC TAC AAG CAA AAC AAG Tyr Thr Glu Leu Ser Asn Ala Lys Ile Ala Tyr Lys Gln Asn Lys 305 310 315	945
GCC AAC ACA GCC CAG GAA CAG CAG TAT GGC AGC CAT GAG GAG AAC Ala Asn Thr Ala Gln Glu Gln Gln Tyr Gly Ser His Glu Glu Asn 320 325 330	990
CTC CCA GCT GAC CTG GAG GCT CTG CAG CGG GAG ATC AGG ATG GCT Leu Pro Ala Asp Leu Glu Ala Leu Gln Arg Glu Ile Arg Met Ala 335 340 345	1035
CAG GAA CGC TTG GAT CTG GCA GTT CAG GCC TAC AGT CAC CAA AAC Gln Glu Arg Leu Asp Leu Ala Val Gln Ala Tyr Ser His Gln Asn 350 355 360	1080
AAC CCT CAT GGT CCC CGG GAG AAG AAG GCC AAA GTG GGG TCC AAA Asn Pro His Gly Pro Arg Glu Lys Lys Ala Lys Val Gly Ser Lys 365 370 375	1125
GCT GGG TCC AAC AAA AGC ACT GCC AGT AGC AAA TCA GGG GAT GGG Ala Gly Ser Asn Lys Ser Thr Ala Ser Ser Lys Ser Gly Asp Gly 380 385 390	1170

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AAG AAC TCT GTC TGG ATT 1188  
 Lys Asn Ser Val Trp Ile  
 395

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Trp	Ser	Phe	Leu	Thr	Arg	Leu	Leu	Glu	Glu	Ile	His	Asn
1				5				10				15		
His Ser Thr Phe Val Gly Lys Ile Trp Leu Thr Val Leu Ile Val														
			20				25					30		
Phe Arg Ile Val Leu Thr Ala Val Gly Gly Glu Ser Ile Tyr Tyr														
			35				40					45		
Asp Glu Gln Ser Lys Phe Val Cys Asn Thr Glu Gln Pro Gly Cys														
			50				55					60		
Glu Asn Val Cys Tyr Asp Ala Phe Ala Pro Leu Ser His Val Arg														
			65				70					75		
Phe Trp Val Phe Gln Ile Ile Leu Val Ala Thr Pro Ser Val Met														
			80				85					90		
Tyr Leu Gly Tyr Ala Ile His Lys Ile Ala Lys Met Glu His Gly														
			95				100					105		
Glu Ala Asp Lys Lys Ala Ala Arg Ser Lys Pro Tyr Ala Met Arg														
			110				115					120		
Trp Lys Gln His Arg Ala Leu Glu Glu Thr Glu Glu Asp Asn Glu														
			125				130					135		
Glu Asp Pro Met Met Tyr Pro Glu Met Glu Leu Glu Ser Asp Lys														
			140				145					150		
Glu Asn Lys Glu Gln Ser Gln Pro Lys Pro Lys His Asp Gly Arg														
			155				160					165		
Arg Arg Ile Arg Glu Asp Gly Leu Met Lys Ile Tyr Val Leu Gln														
			170				175					180		
Leu Leu Ala Arg Thr Val Phe Glu Val Gly Phe Leu Ile Gly Gln														
			185				190					195		
Tyr Phe Leu Tyr Gly Phe Gln Val His Pro Phe Tyr Val Cys Ser														
			200				205					210		
Arg Leu Pro Cys Pro His Lys Ile Asp Cys Phe Ile Ser Arg Pro														
			215				220					225		
Thr Glu Lys Thr Ile Phe Leu Leu Ile Met Tyr Gly Val Thr Gly														
			230				235					240		
Leu Cys Leu Leu Leu Asn Ile Trp Glu Met Leu His Leu Gly Phe														
			245				250					255		
Gly Thr Ile Arg Asp Ser Leu Asn Ser Lys Arg Arg Glu Leu Glu														
			260				265					270		

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGCCTGACT GGACCGCCTT AGGC 24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATCTCGAGG TCATCAGGCC GAGG 24

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAGTTGGA GCTTTCTGAC TCGC 24

(2) INFORMATION FOR SEQ ID NO:10:  
(i) SEQUENCE CHARACTERISTICS

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATCCAGACA GAGTTCTTCC CATC 24

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- (2) INFORMATION FOR SEQ ID NO:11:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGGCGATT GGAGCTTCCT GGGA 24

- (2) INFORMATION FOR SEQ ID NO:12:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGATAGG TCATCTGACC TTGC 24

## WHAT IS CLAIMED IS:

1. A delivery system for delivering a therapeutically effective amount of a predetermined genetic material to an identified cardiac location of a patient's  
5 heart, said genetic material being selected for the function of altering the conductivity of cardiac cells to which it is delivered, comprising:

a supply of said genetic material;  
reservoir means for containing said genetic  
10 material; and

delivery means for delivering said genetic material from said reservoir to said identified cardiac location so as to contact a plurality of cells in the proximity of said cardiac location, thereby changing the  
15 conductivity of said cells and improving the cardiac function of said heart.

2. The delivery system of claim 1, wherein said delivery means comprises a catheter with a distal end having an opening at said distal end, said delivery means  
20 comprising means for delivering said genetic material from said reservoir through said opening, and further comprising:

mapping electrode means positioned at said distal portion for carrying out mapping of the patient's heart so as to identify said cardiac location; and

25 conductor means for connecting said mapping electrode means to the proximal end of said catheter.

3. The delivery system of claim 1, wherein said supply of genetic material comprises a bolus of conduction  
30 protein genetic material selected for the function of enhancing cardiac cell conductivity.

4. The delivery system of claim 1, wherein said delivery means comprises a catheter with a distal end

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portion, and said reservoir means is located in said distal end portion.

5. The delivery system of claim 4, wherein said distal end portion comprises a hollow helical element  
5 forming an interior, and said reservoir means comprises said interior with said supply therein.

6. The delivery system of claim 1, wherein said delivery means comprises a catheter with a lumen for delivering said genetic material therethrough, said catheter  
10 having a distal tip communicating with said lumen for contacting said plurality of cells in the proximity of said cardiac location with said genetic material.

7. The delivery system of claim 6, wherein said distal tip is a hollow helical needle tip.

15 8. The delivery system of claim 6, wherein said catheter is a transvenous endocardial catheter.

9. The delivery system of claim 1, wherein said reservoir contains a supply of 0.1-10 ml of said genetic material.

20 10. The delivery system of claim 1, wherein said delivery means comprises a catheter with a distal portion and an end tip, and wherein said reservoir means is contained in said distal portion, and further comprising force means for forcing said genetic material from said  
25 reservoir means and out of said end tip.

11. The delivery system of claim 10, wherein said force means comprises a stylet.

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12. The delivery system of claim 1, wherein said delivery system comprises a hollow helical screw-in element loaded with a bolus of said genetic material.

13. The delivery system of claim 1, wherein said 5 element comprises ports for egress of said genetic material into said identified cardiac location when said element is screwed into said location, and further comprising soluble plugs in said ports to maintain them normally closed but which dissolve when said element is positioned within said 10 patient's heart.

14. The delivery system of claim 1, wherein said predetermined genetic material is DNA or RNA, and imparts chronic change in conductive properties to said cardiac cells.

15 15. The delivery system of claim 14, wherein said DNA or RNA encodes cardiac gap junction proteins.

16. The delivery system of claim 15, wherein said cardiac gap junction proteins are connexin proteins selected from the group consisting of Cx40, Cx43, and Cx45.

20 17. The delivery system of claim 1, wherein said predetermined genetic material is protein, and imparts acute change in conductive properties to said cardiac cells.

18. The delivery system of claim 17, wherein said protein is cardiac gap junction protein.

25 19. The delivery system of claim 17, wherein said cardiac gap junction proteins are connexin proteins selected from the group consisting of Cx40, Cx43, and Cx45.

20. An implantable delivery system for delivering doses of a therapeutically effective amount of a

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predetermined genetic material to an identified cardiac location, comprising:

a supply of genetic material of the class having the property of altering the conductivity of cardiac cells 5 to which it is delivered;

a catheter, said catheter having a distal tip portion for engaging the cells of said cardiac location and delivering thereto said genetic material;

10 reservoir means for holding said supply of genetic material and providing it to said distal tip portion of said catheter; and

15 delivery means for delivering a therapeutically effective amount of said genetic material from said reservoir means through said distal tip portion to said cardiac location.

21. The system as described in claim 20, further comprising:

20 control means for controlling operation of said delivery means to deliver respective said doses.

22. The implantable delivery system of claim 20, wherein said control means comprises initiating means for initiating delivery of said genetic material, said initiating means comprising an external programmer.

25 23. The implantable delivery system of claim 20, wherein said control means comprises automatic means for automatically initiating delivery of said genetic material.

24. A combined mapping and delivery system for delivering a therapeutically effective amount of a 30 predetermined genetic material to an identified cardiac location of a patient's heart, said genetic material being selected for the function of altering the conductivity of cardiac cells to which it is delivered, comprising:

a supply of said genetic material;

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reservoir means for containing said genetic material;

mapping means for identifying cardiac location within a patient's heart; and

5 delivery means within said mapping means for delivering said genetic material from said reservoir to said identified cardiac location so as to contact a plurality of cells in the proximity of said cardiac location, thereby changing the conductivity of said cells and improving the  
10 cardiac function of said heart.

25. The combined mapping and delivery system of claim 24, wherein said mapping means comprises a catheter or peelable introducer sheath having two electrodes and said delivery means comprises a catheter having a distal end  
15 portion comprising a hollow helical element.

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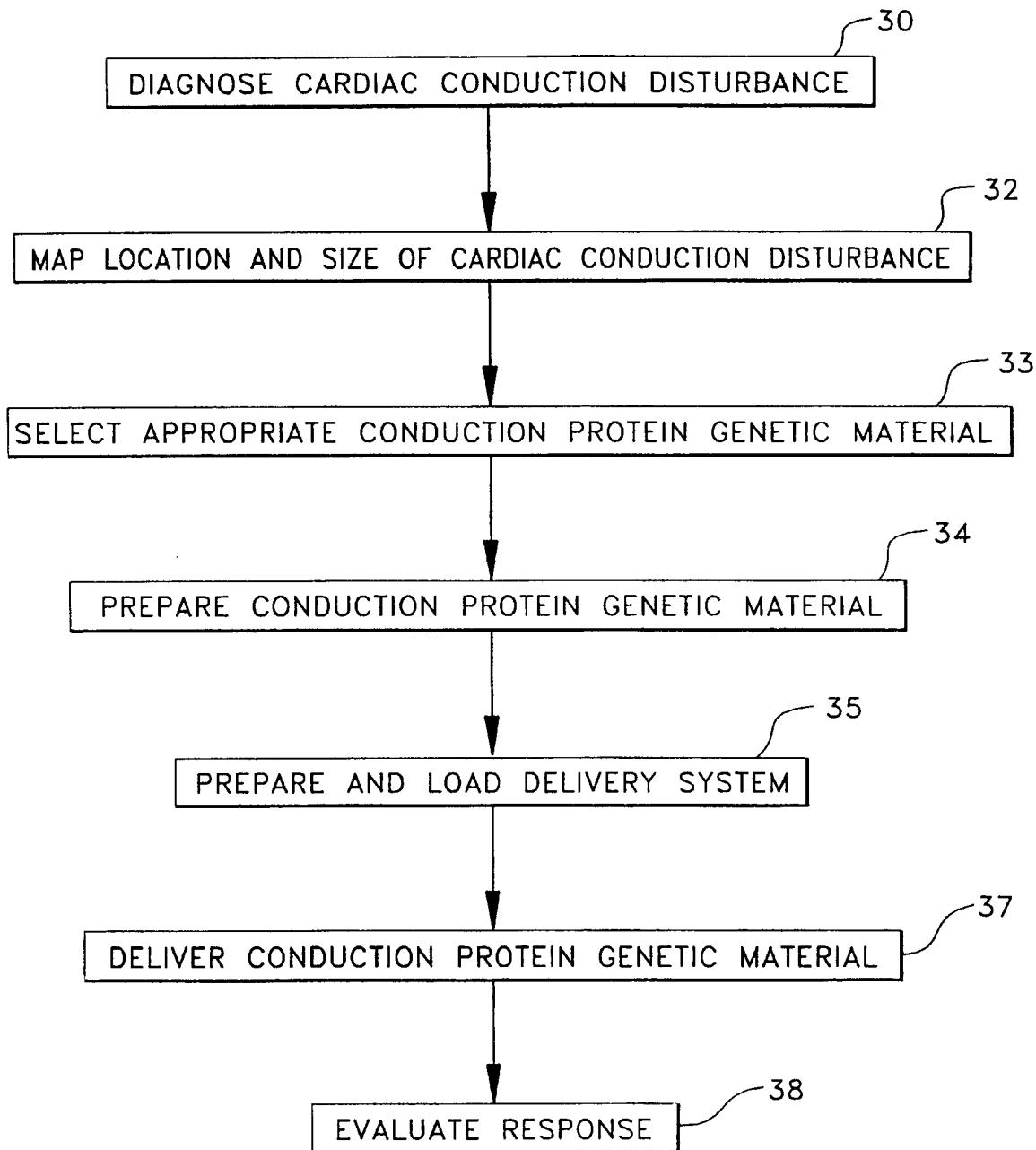


FIG. 1

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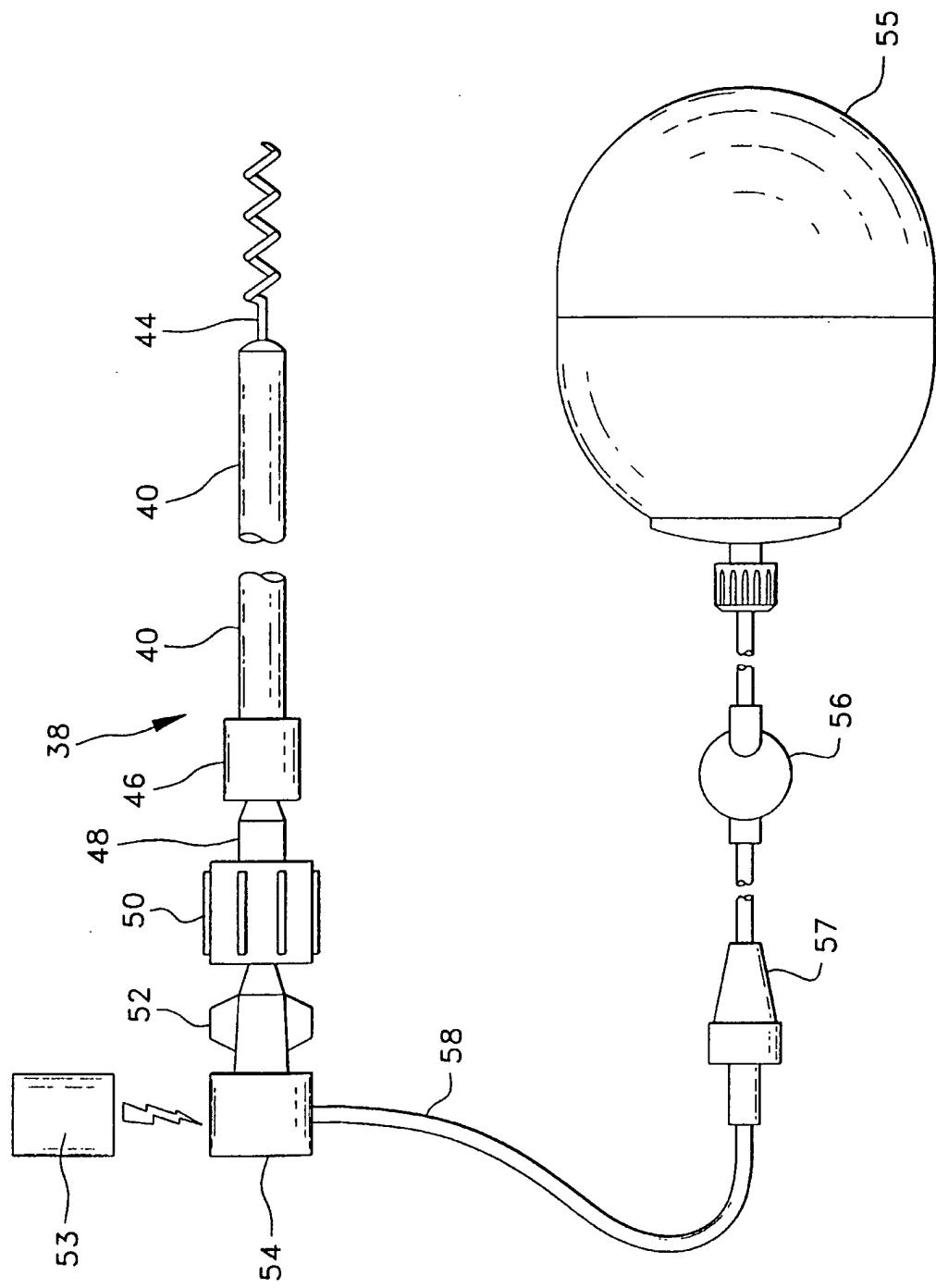


FIG. 2

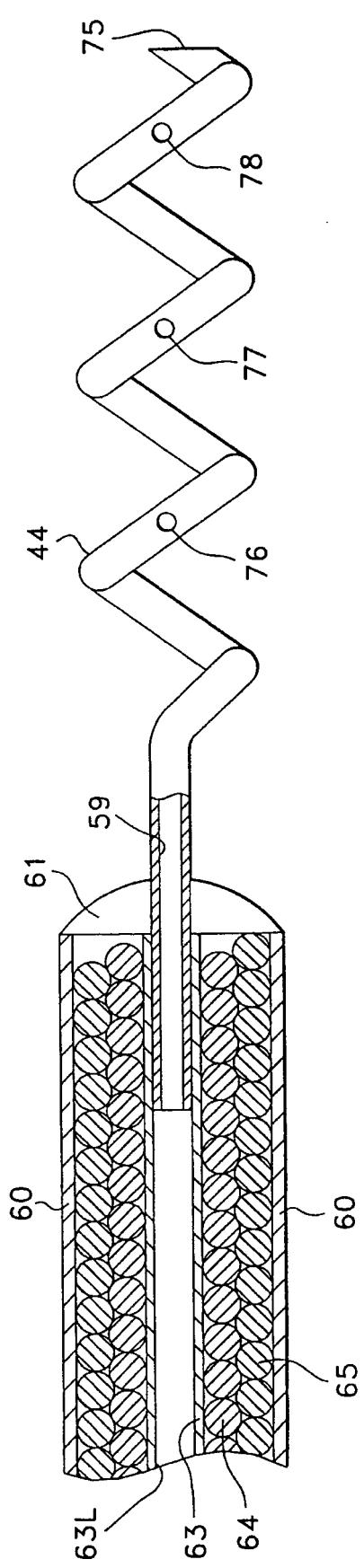


FIG. 3

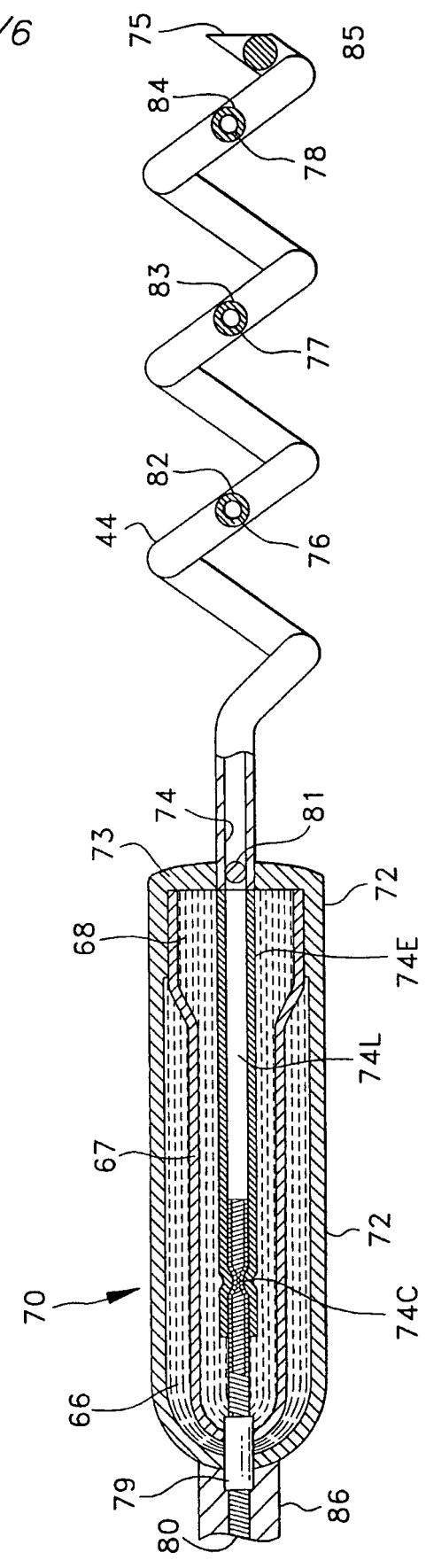


FIG. 4

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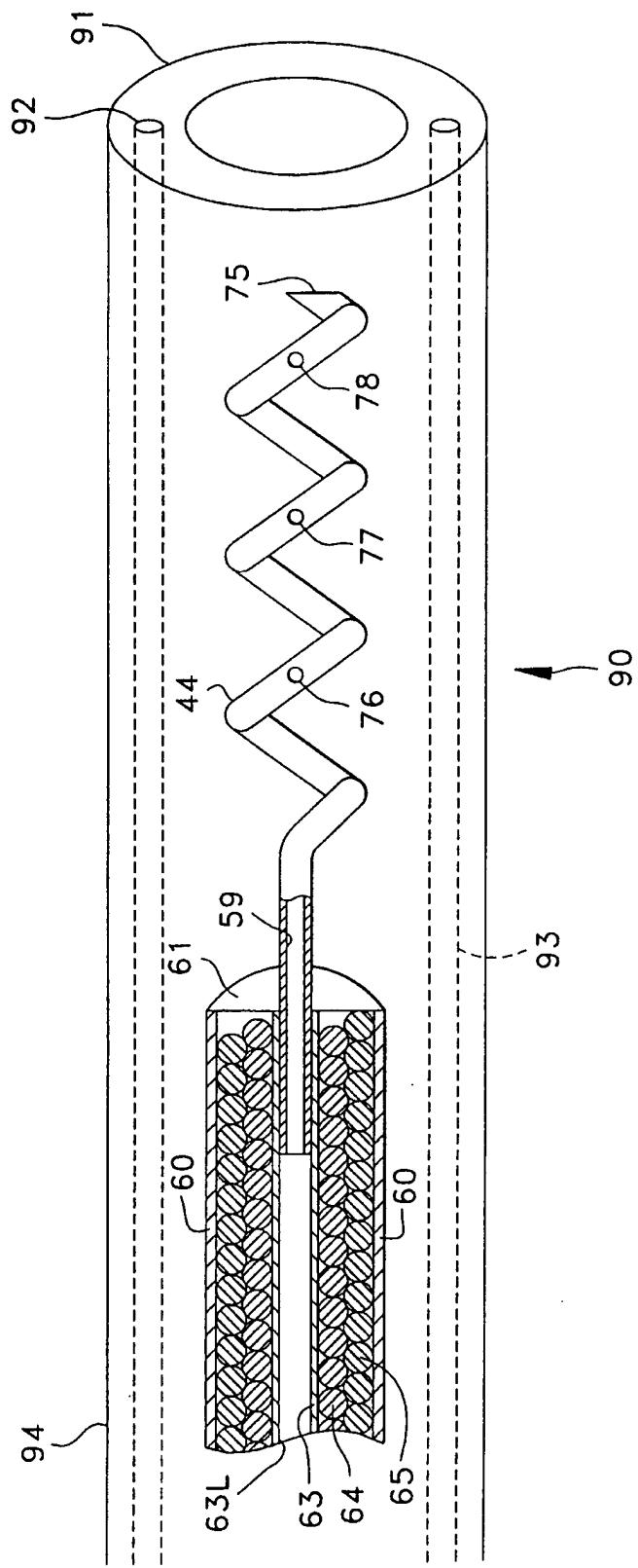


FIG. 5

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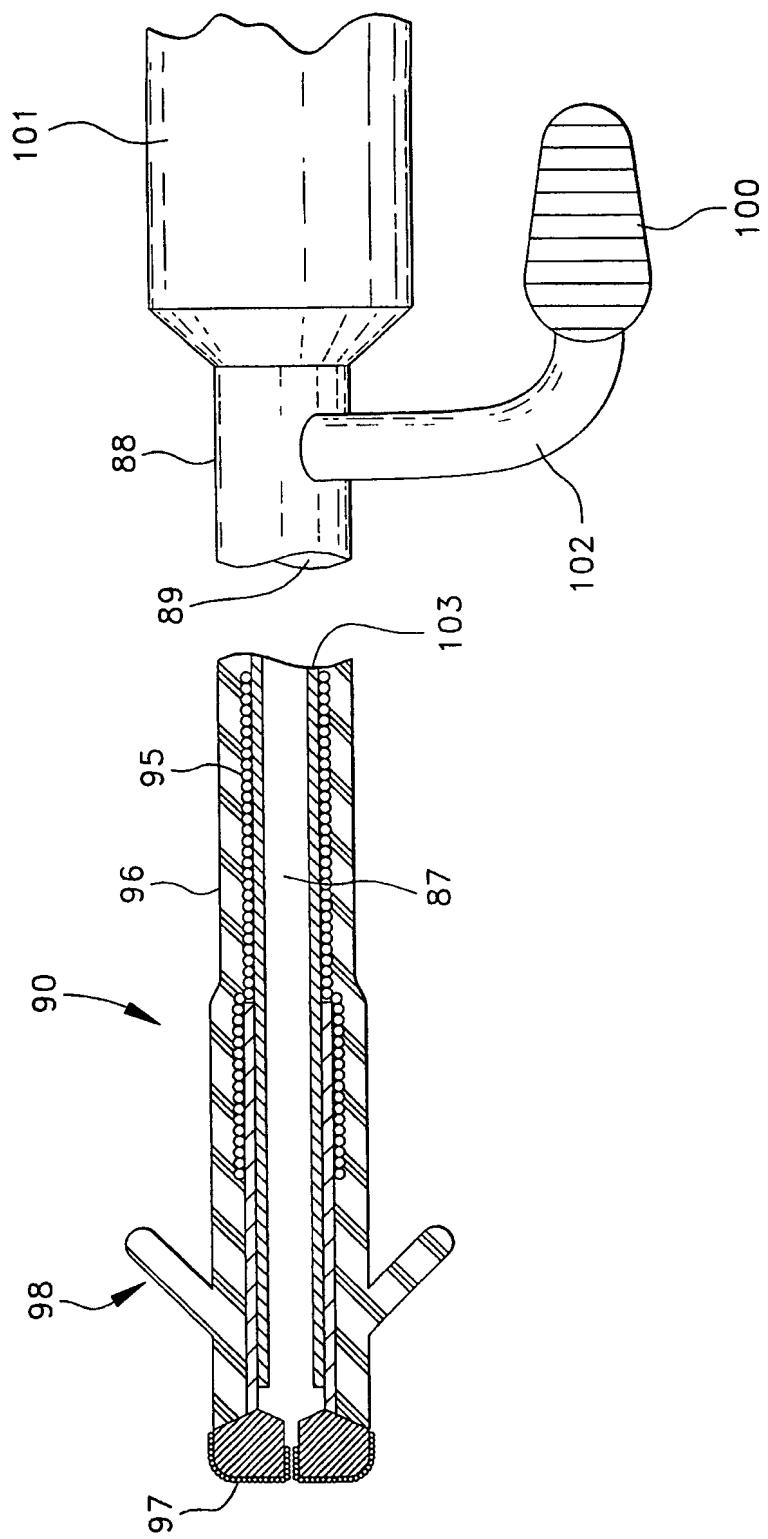


FIG. 6A

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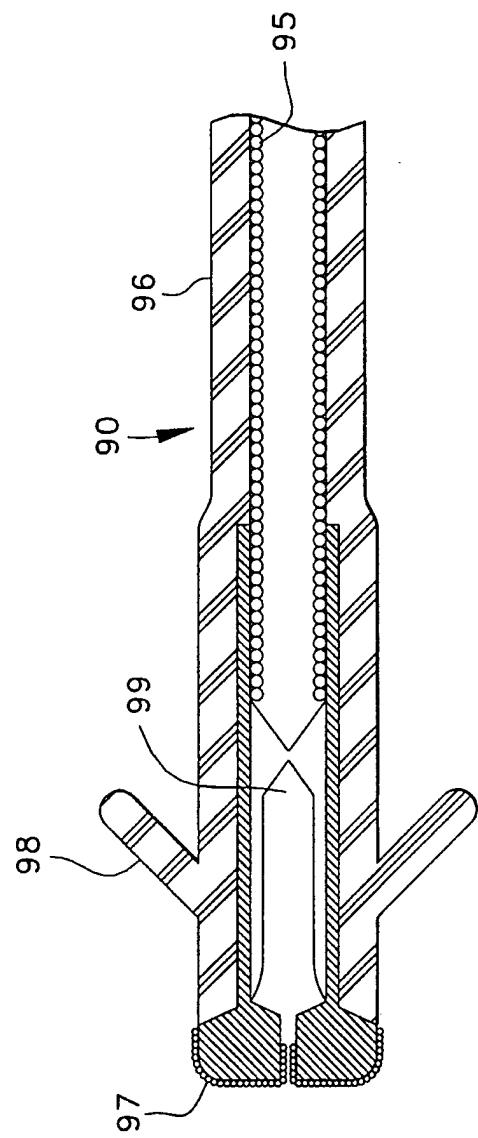


FIG. 6B

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/06103

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : A61K 31/00; A01N 43/04; C07H 21/04  
US CL : 604/53; 514/44; 536/23.5

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 604/53; 514/44; 536/23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

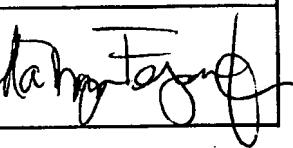
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 94/11506 A1 (ARCH DEVELOPMENT CORPORATION) 26 May 1994, see entire document.	1-25
Y	US 5,328,470 A (NABEL ET AL.) 12 July 1994, see entire document.	1-25
Y	FISHMAN et al. Molecular Characterization and Functional Expression of the Human Cardiac Gap Junction Channel. J. Cell Biol. August 1990, Vol. 111, pages 589-598, see entire document.	1-25
Y	KANTER et al. Molecular Cloning of Two Human Cardiac Gap Junction Proteins, Connexin40 and Connexin45. J. Mol. Cell Cardiol. 1994, Vol. 26, pages 861-868, see entire document.	1-25

<input checked="" type="checkbox"/>	Further documents are listed in the continuation of Box C.	<input type="checkbox"/>	See patent family annex.
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20 MAY 1997	09 JUN 1997
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer  CHRISTOPHER S. F. LOW Telephone No. (703) 308-0196
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## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/06103

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 95/05781 A1 (MEDTRONIC, INC.) 02 March 1995, see entire document.	1-25
Y	WO 93/04724 A1 (MEDTRONIC, INC.) 18 March 1993, see entire document.	1-25
Y	GOURDIE et al. The spatial distribution and relative abundance of gap-junctional connexin40 and connexin43 correlate to functional properties of components of the cardiac atrioventricular conduction system. J. Cell Sci. 1993, Vol. 105, pages 985-991, see entire document.	1-25

**INTERNATIONAL SEARCH REPORT**

International application No.  
PCT/US97/06103

**B. FIELDS SEARCHED**

Electronic data bases consulted (Name of data base and where practicable terms used):

Automated Patent System - USPAT, JPOABS, EPOABS

DIALOG - MEDLINE

Search terms: catheter cardiac stylet gap junction dna protein cx40 cx43 cx45 mapping

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